

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 15:01:02 ; Search time 177 Seconds
(without alignments)
1886.303 Million cell updates/sec

Title: US-10-614-076-98

Perfect score: 3406

Sequence: 1 MNPNNRSEHTIKVPENSEL.....SFVSNKVIYDKIEFIPVOL 652

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	652	1	C3BB_BACTU
2	3212	94.3	659	1	C3BA_BACTO
3	2341.5	68.7	644	1	C3AA_BACTT
4	2341.5	68.7	652	2	Q9SGN9
5	2337.5	68.6	652	2	Q6PXN8
6	2319.5	68.1	652	2	Q643Z7
7	2152	63.2	649	1	C3CA_BACTK
8	1272.5	37.4	1144	2	Q8KZL7
9	1205.5	35.4	1157	1	C8AA_BACUK
10	1166.5	34.2	1159	1	C8BA_BACUK
11	1127.5	33.1	1157	1	C9CA_BACTO
12	1124.5	33.0	719	1	C1IB_BACTE
13	1122	32.9	1223	1	C1BB_BACTU
14	1122	32.9	1233	1	C1BC_BACTM
15	1121	32.9	1215	1	C1KA_BACTM
16	1119	32.9	1138	1	C7AA_BACTU
17	1118.5	32.8	719	2	Q9F0P8
18	1117	32.8	1138	1	C7AB_BACUK
19	1115.5	32.8	719	1	C1ID_BACTU
20	1112	32.6	1138	1	C7AB_BACUA
21	1100.5	32.3	719	1	C1IA_BACTK
22	1100.5	32.3	719	2	Q93N75
23	1100.5	32.3	719	2	Q6X181
24	1096.5	32.2	719	2	Q8K761
25	1094.5	32.1	719	2	O85796
26	1072.5	31.5	1228	1	C1BA_BACTK
27	1071.5	31.5	1228	2	Q93N75
28	1070.5	31.4	1228	2	Q93T75
29	1060	31.1	1160	1	C8CA_BACTP
30	1060	31.1	1160	2	Q6R2R6
31	1053	30.9	1231	2	Q8KNY2

32	1046.5	30.7	719	1	C1IC_BACTU	O87404 bacillus th
33	1042	30.6	1231	1	C1BD_BACTZ	O92a25 bacillus th
34	1041.5	30.6	1159	1	C9DA_BACTP	O6014 bacillus th
35	1018	29.9	1154	2	Q6QAN9	O6qan9 bacillus th
36	1013	29.7	849	2	Q6PYW8	O6pyw8 bacillus th
37	1013	29.7	1227	1	C1BE_BACTU	O85805 bacillus th
38	999.5	29.3	645	2	Q9S603	O8s603 bacillus th
39	995	29.2	1150	1	C9EA_BACTA	O92n19 bacillus th
40	995	29.2	1150	2	Q71RP4	Q71rp4 bacillus th
41	975	28.6	1163	1	CQAA_BACTP	Q9x597 bacillus th
42	963.5	28.3	1144	2	Q45745	Q45745 bacillus th
43	934.5	27.4	1189	1	C1CA_BACTE	P05518 bacillus th
44	934.5	27.4	1189	2	Q6YNN8	Q6ynb8 bacillus th
45	932.5	27.4	1189	2	Q9L877	Q9l877 bacillus th
46	909	26.7	793	2	Q6PYW7	Q6pyw7 bacillus th
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48	899.5	26.4	1155	2	Q7BE98	Q7be98 bacillus th
49	899.5	26.4	1155	2	Q9F296	Q9f296 bacillus th
50	898.5	26.4	1156	2	Q6GUA7	Q6gua7 bacillus th
51	898.5	26.4	1174	1	C1FA_BACTA	Q03746 bacillus th
52	897	26.3	1118	2	Q9AM63	Q9am63 bacillus th
53	893.5	26.2	1177	2	Q6EIX3	Q6eix3 bacillus th
54	891.5	26.2	1155	2	Q93T21	Q93t21 bacillus th
55	888	26.1	1181	1	C1AE_BACTL	Q03748 bacillus th
56	886.5	26.0	1176	1	C1CB_BACTG	P56953 bacillus th
57	883.5	25.9	1179	1	C1AD_BACTA	Q03744 bacillus th
58	876	25.7	1176	2	Q7WZT9	Q7wz29 bacillus th
59	874	25.7	1180	2	Q9SSV8	Q9ssv8 bacillus th
60	873.5	25.6	1171	2	O06894	O06894 bacillus th
61	870	25.5	620	2	Q45720	Q45720 bacillus th
62	870	25.5	1176	2	Q45736	Q45736 bacillus th
63	869.5	25.5	1171	1	C1EA_BACTX	O54758 bacillus th
64	869.5	25.5	1171	2	Q71TM6	Q71tm6 bacillus th
65	867.5	25.5	1177	2	Q45735	Q45735 bacillus th
66	867.5	25.5	1177	2	Q8GLY5	Q8gly5 bacillus th
67	867	25.5	1178	1	C1AC_BACTK	P05068 bacillus th
68	867	25.5	1178	2	Q6XLN7	Q6xln7 bacillus th
69	866.5	25.4	1166	1	C1GA_BACTU	O45746 bacillus th
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71	865.5	25.4	829	2	Q6BE06	Q6be06 bacillus th
72	865	25.4	1176	2	Q9RC30	Q9rc30 bacillus th
73	863	25.3	1178	2	Q9R826	Q9r826 bacillus th
74	862	25.3	618	2	Q32306	Q32306 bacillus th
75	861.5	25.3	607	2	Q45721	Q45721 bacillus th
76	861.5	25.3	618	2	Q45737	Q45737 bacillus th
77	861.5	25.3	723	2	Q9S4B5	Q9s4b5 bacillus th
78	861.5	25.3	1177	2	Q03743	Q03743 bacillus th
79	861.5	25.3	1177	2	Q71JF1	Q71jf1 bacillus th
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82	854.5	25.1	1169	2	O8GHE8	Q8ghe8 bacillus th
83	850.5	25.0	1169	1	C1GB_BACTZ	Q92a26 bacillus th
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85	845	24.8	1174	2	Q45749	Q45749 bacillus th
86	844	24.8	1167	1	C1JA_BACTU	Q45738 bacillus th
87	841	24.7	648	1	CJAA_BACTJ	O32307 bacillus th
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89	838	24.6	793	2	Q6PYW9	Q6pyw9 bacillus th
90	835	24.5	1174	1	C1EB_BACTA	Q03745 bacillus th
91	828	24.3	1160	2	C1DB_BACTU	Q45747 bacillus th
92	828	24.3	1160	2	Q93TF9	Q93tf9 bacillus th
93	821	24.1	825	2	Q6BE09	O6be09 bacillus th
94	816	24.0	1332	2	Q765X5	Q765x5 paenibacill
95	811.5	23.8	660	2	Q8RQU6	Q8rqv6 paenibacill
96	810.5	23.8	1118	2	Q9AM82	Q9am82 bacillus th
97	807	23.7	1176	2	Q9S514	Q9s514 bacillus th
98	805.5	23.6	1344	2	Q765X7	Q765x7 paenibacill
99	797.5	23.4	782	2	Q6PYW6	Q6pyw6 bacillus th
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101	788	23.1	1155	1	C1HE_BACTM	Q45718 bacillus th
102	787.5	23.1	1172	1	C1HA_BACTU	Q45748 bacillus th
103	783	23.0	1176	1	C1AG_BACTU	Q9s515 bacillus th
104	773.5	22.7	686	2	Q75QQ5	Q75qq5 bacillus th

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129 535 15.7 675 1 C9AA_BACTU 129 535 15.7 675 1 C9AA_BACTU
130 534 15.7 826 1 C9AA_BACTU 130 534 15.7 826 1 C9AA_BACTU
131 520 15.3 618 1 CHAA_CLOBI 131 520 15.3 618 1 CHAA_CLOBI
132 483 14.2 1155 2 Q9AM80 132 483 14.2 1155 2 Q9AM80
133 482 14.2 613 1 CGAA_CLOBI 133 482 14.2 613 1 CGAA_CLOBI
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135 316 9.3 1257 1 C9AA_BACTU 135 316 9.3 1257 1 C9AA_BACTU
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137 279.5 8.2 1245 1 CSBA_BACTU 137 279.5 8.2 1245 1 CSBA_BACTU
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139 272.5 8.0 1167 1 CLAA_BACTU 139 272.5 8.0 1167 1 CLAA_BACTU
140 262 7.7 633 1 C2AD_BACTU 140 262 7.7 633 1 C2AD_BACTU
141 255.5 7.5 196 2 Q6S554 141 255.5 7.5 196 2 Q6S554
142 251.5 7.4 633 2 Q6RPF60 142 251.5 7.4 633 2 Q6RPF60
143 248.5 7.3 633 2 Q9S6N5 143 248.5 7.3 633 2 Q9S6N5
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146 245.5 7.2 633 1 C2AA_BACTK 146 245.5 7.2 633 1 C2AA_BACTK
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Q9AM81 bacillus th
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O8VUK9 bacillus th
O9Y031 bacillus th
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O05102 clostridium
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Q7X2S7 bacillus th

Appl. Environ. Microbiol. 58:3921-3927(1992).
[2]
SEQUENCE FROM N.A.
STRAIN=NRRL B-18655 / EG5144;
Donovan W.P., Rupar M.J., Slaney A.C.;
" Bacillus thuringiensis cryIIIC, (b) protein toxic to coleopteran
insects.";
Patent number US5378625, 03-JAN-1995.
-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
epithelial cells of Coleoptera. Has moderate level of toxicity to
southern corn rootworm.
-!- SUBUNIT: Monomer.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
-!- SIMILARITY: Belongs to the delta endotoxin family.
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EMBL; M89794; AAA22334.1; -.
EMBL; U31633; AAA74198.1; -.
PIR; I39811; I39811.
PDB; 1J16; X-ray; A=64-652.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_Like.
Pfam; PF00555; Endotoxin M; 1.
Pfam; PF03944; Endotoxin C; 1.
Pfam; PF03945; Endotoxin N; 1.
3D-structure; Sporulation; Toxin.
VARIANT 21 21 Q -> P (in strain EG5144).
VARIANT 97 97 N -> D (in strain EG5144).
VARIANT 289 289 I -> V (in strain EG5144).
VARIANT 352 352 F -> S (in strain EG5144).
VARIANT 417 419 VYL -> IYF (in strain EG5144).
VARIANT 451 451 S -> G (in strain EG5144).
VARIANT 590 590 L -> I (in strain EG5144).
VARIANT 600 600 K -> I (in strain EG5144).
VARIANT 624 624 K -> T (in strain EG5144).
HELIX 65 79
TURN 80 81
HELIX 83 86
TURN 87 88
TURN 91 98
TURN 99 99
TURN 102 103
TURN 105 113
TURN 114 114
TURN 115 118
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TURN 210 210
TURN 211 215
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HELIX 281 281

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ALIGNMENTS

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RESULT 1
C3BB_BACTU
ID C3BB_BACTU STANDARD; PRT; 652 AA.
AC Q06117; Q45717;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pesticidal crystal protein cry3Bb (insecticidal delta-endotoxin
DE CryIIIB(b)) (Crystalline entomocidal protoxin) (74 kDa crystal
DE protein).
GN Name=cry3Bb; Synonyms=cryIIIB(b), cryIIIB2;
OS Bacillus thuringiensis;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG4961;
RX MEDLINE=93119147; PubMed=1476436;
RA Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke M.C.,
RA Johnson T.B.;
RT "Characterization of two genes encoding Bacillus thuringiensis
RT insecticidal crystal proteins toxic to Coleoptera species.";

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FT TURN 282 283
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FT STRAND 625 631
FT TURN 636 637
FT STRAND 640 649
SQ SEQUENCE 652 AA; 74385 MW; 63048332CDB8CCC6 CRC64;

Query Match 100.0%; Score 3406; DB 1; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.3e-214;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKVTNPSELQTHNQYPLADNPSTLEELNYKEFLRMTEDSDSTEVLDS 60
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DB 61 TVKDAVGTGIVSVGQILGVGVFPAGALTIFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
QY 121 KIBEYAKSALAELOGLQNNFEDYVNALNSWKKTPLSLRKRSQDRIRLFSAQESHFRN 180
DB 121 KIBEYAKSALAELOGLQNNFEDYVNALNSWKKTPLSLRKRSQDRIRLFSAQESHFRN 180
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DB 181 SMPSFAVSKFEVLFLPTYAQAAANTHLLLLKDAQVFGEEWGYSSSEDVAEFYHROLKLTQY 240

241 TDHCVMWYVGLNGLRGSTYDAWKFNRFREMTLTVLDLIVLPFFDIRLYSGVKTEL 300
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361 SGNVETRPSIGSKTITSPFYGDKSTPEVKLSFDGQKVYRTIANTDVAWPNKGYVLG 420
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421 VTKVDFSQYDDQKNETSTQYDSKRNNGHVSAODSIDQLPPTTDEPLEKAYSHQLNYAE 480
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541 LFLKESNSIAKEKVTLSAALLQRYVRIRYASTTNLRLPVQNSNDELVIYINKTMNK 600
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601 DDLTYQTFLATNSNMFGSGDKNELIIGAESFVSNEKIYIDKIEFIPVOL 652
601 DDLTYQTFLATNSNMFGSGDKNELIIGAESFVSNEKIYIDKIEFIPVOL 652

RESULT 2
C3BA_BACTO
ID C3BA_BACTO STANDARD; PRT; 659 AA.
AC P17969;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry3Ba (Insecticidal delta-endotoxin
DE CryIIIB(a)) (Crystalline entomocidal protoxin) (75 kDa crystal
DE protein)
GN Name=cry3Ba; Synonyms=cryIIB, cryIIIB(a);
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=43F;
RX MEDLINE=90206811; PubMed=2320431;
RA Sick A., Gaertner F.H., Wong A.;
RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
RT isolate of Bacillus thuringiensis subsp. tolworthi.";
RL Nucleic Acids Res. 18:1305-1305(1990).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X17123; CAA34983.1; --
CC EMBL; A07234; CAA00645.1; --
CC PIR; S10228; S10228.
CC HSSP; Q06117; 1J16.
CC InterPro; IPR001178; Endotoxin.

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DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
KW Sporulation; Toxin. 75159 MW; 5ASB214FP94168CA CRC64;
SQ SEQUENCE 659 AA; 75159 MW; 5ASB214FP94168CA CRC64;

Query Match          94.3%; Score 3212; DB 1; Length 659;
Best Local Similarity 93.7%; Pred. No. 1.2e-201;
Matches 610; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 1 MNPNNRSHDITKVTNPSELQNHQYPLADNPSTLEELNYKEPLRMTESSTVELDNS 60
DB 9 MNPNNRSEYDITKVTNPSELQNHQYPLADNPSTLEELNYKEPLRMTADNSTEVLDS 68

QY 61 TVKDAVGTGISVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVFLVDK 120
DB 69 TVKDAVGTGISVVGQILGVGVPPFAGALTSFYQSFLNAINWSDADPWKAFMAQVFLVDK 128

QY 121 KIEEYAKSKALAELOGLQNNFEDYNNALNSWKKTPLSLRSKRQDRIRELFSQAESHFRN 180
DB 129 KIEEYAKSKALAELOGLQNNFEDYNNALNSWKKAPVNLRSRQDRIRELFSQAESHFRN 188

QY 181 SMPFAVSKFEVLPLPTTAAQAANTHLLLLKDAQVGEWGYSSEDAVFYHROLKLTQOY 240
DB 189 SMPFAVSKFEVLPLPTTAAQAANTHLLLLKDAQVGEWGYSSEDAVFYHROLKLTQOY 248

QY 241 TDHCNVNNGVNLGRGSTDYDAWVFNRRREMTLTVLDLIVLFFDYDIRLYSKGVKTTEL 300
DB 249 TDHCNVNNGVNLGRGSTDYDAWVFNRRREMTLTVLDLIVLFFDYDIRLYSKGVKTTEL 308

QY 301 TRDIFTDPIFSLNTLOEYGPFTFLSIENSRKPHLFDYLGIEFHTRLQPGYFGKDSFNYW 360
DB 309 TRDIFTDPIFSLNTLOEYGPFTFLSIENSRKPHLFDYLGIEFHTRLQPGYFGKDSFNYW 368

QY 361 SGNYVETRPSIGSSKTIISPFYGDKSTPEVKLSFDGQKVVTIANTDVAAPNPKGVVIG 420
DB 369 SGNYVETRPSIGSSKTIISPFYGDKSTPEVKLSFDGQKVVTIANTDVAAPNPKGVVIG 428

QY 421 VTKVDFPSQYDDQKNETSTQYDSKNNHGVSAQDSIDQLPPTTDEPLEKAYSHQNLVAE 480
DB 429 VTKVDFPSQYDDQKNETSTQYDSKRYNGVLAQDSIDQLPPTTDEPLEKAYSHQNLVAE 488

QY 481 CFLMDRRGTIPFFTWTHRSVDFNTIDAETITQLPVVYAYALSSGASIEEGPGTGGNL 540
DB 489 CFLMDRRGTIPFFTWTHRSVDFNTIDAETITQLPVVYAYALSSGASIEEGPGTGGNL 548

QY 541 LFLKSSNSIAKPKVTLNSAALLQVRVIRVASTTNLRLFVQNSNNDPLVIYINKTNMK 600
DB 549 LFLKSSNSIAKPKVTLNSAALLQVRVIRVASTTNLRLFVQNSNNDPLVIYINKTNMK 608

QY 601 DDDLTVTQTDPLATNSNMFGSDGNELIIGASFSVSNEXIYDKIEFIPVQ 651
DB 609 DGDLTVTQTDPLATNSNMFGSDGTDNFIIGASFSVSNEXIYDKIEFIPVQ 659

RESULT 3
C3AA_BACTT STANDARD; PRT; 644 AA.
AC P07130; P21255;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-
DE endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa
DE crystal protein).
GN Name=cry3Aa; Synonyms=bt13, cry3A, cryC, cryIIIA, cryIIIA(a);
OS Bacillus thuringiensis (subsp. tenebrionis);
OS Bacillus thuringiensis (subsp. morrisoni); and
OS Bacillus thuringiensis (subsp. san diego).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
```

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OX NCBI_TaxID=1444, 1441, 1435;
RN [1]
RN SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RX MEDLINE=88015559; PubMed=3658680;
RA Hoesfte H., Seurinck J., Houtven A.V., Vaeck M.;
RT "Nucleotide sequence of a gene encoding an insecticidal protein of
RT Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";
RL Nucleic Acids Res. 15:7183-7183(1987).
RN [2]
RN SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA Sekar V., Thompson D.V., Maroney M.J., Bookland R.G., Adang M.J.;
RT "Molecular cloning and characterization of the insecticidal crystal
RT protein gene of Bacillus thuringiensis var. tenebrionis.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
RN [3]
RN SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavrik P.B.,
RA Fischhoff D.A.;
RT "Characterization of the coleopteran-specific protein gene of Bacillus
RT thuringiensis var. tenebrionis.";
RL Biotechnology (N.Y.) 6:61-66(1988).
RN [4]
RN SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis; STRAIN=NB176;
RX MEDLINE=95131759; PubMed=7830581;
RA Adams L.F., Mathewes S., O'Hara P., Petersen A., Gurtler H.;
RT "Elucidation of the mechanism of CryIIIA overproduction in a
RT mutagenized strain of Bacillus thuringiensis var. tenebrionis.";
RL Mol. Microbiol. 14:381-389(1994).
RN [5]
RN SEQUENCE FROM N.A.
RC SPECIES=B.t.morrisoni; STRAIN=EG2158;
RX MEDLINE=89112139; PubMed=3146015;
RA Donovan W.P., Gonzalez J.M. Jr., Gilbert M.P., Dankocsik C.C.;
RT "Isolation and characterization of EG2158, a new strain of Bacillus
RT thuringiensis toxic to coleopteran larvae, and nucleotide sequence of
RT the toxin gene.";
RL Mol. Gen. Genet. 214:365-372(1988).
RN [6]
RN SEQUENCE FROM N.A.
RC SPECIES=B.t.san diego;
RX MEDLINE=88112860; PubMed=1658659; DOI=10.1016/0378-1119(87)90174-0;
RA HERNSTADT C., GILROY T.E., SOBIECKI D.A., BENNETT B.D.,
RA GAERTNER F.H.;
RT "Nucleotide sequence and deduced amino acid sequence of a coleopteran-
RT active delta-endotoxin gene from Bacillus thuringiensis subsp. san
RT diego.";
RL Gene 57:37-46(1987).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC SPECIES=B.t.tenebrionis;
RX MEDLINE=92049729; PubMed=1658659; DOI=10.1038/353815a0;
RA Li J., Carroll J., Ellar D.J.;
RT "Crystal structure of insecticidal delta-endotoxin from Bacillus
RT thuringiensis at 2.5-A resolution.";
RL Nature 353:815-821(1991).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
CC insect-resistant potato by Monsanto.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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EMBL; Y00420; CAA68482.1; -	
EMBL; J02978; ARA22541.1; -	
EMBL; M37207; AAN50255.1; -	
EMBL; U10985; AAC43466.1; -	
EMBL; M30503; AAR22542.1; -	
EMBL; M22472; AAA22336.1; ALT INIT.	
PDB; 1DCL; X-ray; @=61-644.	
InterPro; IPR001178; Endotoxin.	
InterPro; IPR005638; endotoxin_C.	
InterPro; IPR005639; endotoxin_N.	
InterPro; IPR008979; Gal_bind_Like.	
Pfam; PF03944; Endotoxin_C; 1.	
Pfam; PF00555; Endotoxin_M; 1.	
Pfam; PF03945; Endotoxin_N; 1.	
3D-structure; Genetically modified food; Sporulation; Toxin.	
PROPEP 1 57	Removed in mature form.
CHAIN 58 644	
CONFLICT 544 544	Pesticidal crystal protein cry3Aa. G -> A (in Ref. 3).

FT	TURN .	500	501
FT	STRAND	503	504
FT	STRAND	509	513
FT	HELIX	514	516
FT	STRAND	519	520
FT	TURN	522	523
FT	STRAND	525	527
FT	STRAND	537	540
FT	STRAND	544	550
FT	STRAND	552	553
FT	STRAND	560	569
FT	STRAND	573	579
FT	TURN	580	581
FT	STRAND	582	589
FT	TURN	595	596
FT	HELIX	601	603
FT	STRAND	605	608
FT	STRAND	613	614
FT	STRAND	619	625
FT	TURN	629	630
FT	STRAND	633	644
SQ	SEQUENCE	644 AA; EFCEPF1CEEFDA9683 CRC64;	

Query Match		68.7%; Score 2341.5; DB 1; Length 644;
Best Local Similarity		68.6%; Pred. No. le-14;
Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;		

Qy	1	MNPNNRSEHDTIKVTPNSELOTNHNQYPLADPNSTLEELANYKEFURMTEDSSTEVLDNS	60
Dd	1	MNPNNRSEHDTIKTENNEVPTHRVQVPLAETFPNTLEDLNYKEFURMTADNTEALDSS	60
		: : : : : : : : : :	
Qy	61	TVKDAVGTSISGVGQILGVGVFPAGALTFSFYOSFLNTIWPSDADPWKAPMAQVEVLIDK	120
Dd	61	TTKDVIQKGISVVDLLGVGVFPFGCALYSFYTNFLTINWPSB-DPWKAPEMEQVEALMDQ	119
		: : : : : : : : :	
Qy	121	KIBEYAKSKALAEQLQGNNFEDYVNALNSWKKTPLSLRSKRSDRIREFLSQAESHFRN	180
Dd	120	KIADYAKNKALAEQLQGNNVEDYVSALSWSQKNPVSSRRPHSQGRIRELFPSQAESHFRN	179
		: : : : : : : : :	
Qy	181	SMSPFAVSKEVLPLPTYAQAAANTHLILLKDAQVFGEENGYSSEDVAEFVHRQLKLTOOY	240
Dd	180	SMSPFAISGYEVLPPTYAQAAANTHLFLKDAQIYGEEWGYEKEDIAEFYKRLQLTQEY	239
		: : : : : : : : :	
Qy	241	TDHCVMYNVGLNGLRGSTYDAMVKFNRRFRREMTLTVDLIIVLPFYDIRLYSKGVKTEL	300
Dd	240	TDHCVMYNVGLDKLRGSYESWNRYRREMTLTVDLIAIFPLYDVRLYPKEVKTEL	299
		: : : : : : : : :	
Qy	301	TRDIPTDPIFSNLTAQEGYGTFFPUSIENSRKPPLFDYLOGIEPHTRLQPGYFGKDSFNW	360
Dd	300	TRDVLTDPIGVNVRGSGYTFSNIENIRKPKHPFDYLHRIQPHTRFQPGYGNDSFNW	359
		: : : : : : : : :	
Qy	361	SGNYVETRPSIGSSKITPPFYGDCKSTEPQVKLSFGQKVYRTIANTVAMPNGKVYLG	420
Dd	360	SGNYVETRPSIGSNDITGPFGYGNKSSEPVQNLEFNGEKYKYRAVANTLAVMPSA-VYSG	418
		: : : : : : : : :	
Qy	421	VTKVDFQSQQDNKETSTOTYDSKRNHGVSAODSIDQLPETTTDEPLEKAYSHQLNVAE	480
Dd	419	VTKVESQYNDQDEASTQTYSKRNVGAVS-WDSIDQLPETTTDEPLEKAYSHQLNVAE	477
		: : : : : : : : :	
Qy	481	CFLMQDRRGTIPTFTWTHRSDVFNTIDAEDITQLPWWKAYALSSGASIEGPGFTGGNL	540
Dd	478	CFLMQGSRGTIPVLTWTHKSVDFNMIDSKKITQLPLVKAYKLQSCASVVAGPRFTGGDI	537
		: : : : : : : : :	
Qy	541	LFLKESNSIAKFVTNLNSAALLQRVVRIRVASTNTNRLFVQNSNNDLVIIYINTMKK	600
Dd	538	IQCETE-NGSAATITYVT-PDVSYSQKYRARIHVASTSQITFTLSLDGAPFNQYFDKINK	595
		: : : : : : : : :	
Qy	601	DDDLTYQTDLATTNSMFGSDGNELIIGAESFVSNKIYIDKIEFIPV	650
Dd	596	GDTLTNTSNFLASFSTPFELSG--NNLQIGVTGLSAGDKVIIDKIEFIPV	643
		: : : : : : : : :	

RESULT 4

```
Q9SGN9 ID Q9SGN9 PRELIMINARY; PRT; 652 AA.
AC Q9SGN9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Cry3Aa protein.
GN Name=cry3Aa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]_TaxID=1428;
RP SEQUENCE FROM N.A.
RC STRAIN=Bt22;
RA Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; A2737900; CAB41411.1; -.
DR PIR; A27323; A27323.
DR HSP; P07130; IDLC.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 652 AA; 74035 MW; 544AE16E1DDF7647 CRC64;

Query Match 68.7%; Score 2341.5; DB 2; Length 652;
Best Local Similarity 68.6%; Pred. No. 1.9e-144;
Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;

QY 1 MNPNNRSHDTIKVTNPSELQTNHNYPLADNPNSTLELNKYKEFLRMTESSSTEVLDS 60
DB 9 MNPNNRSHDTIKVTENNEVPTNHVQYPLAETPNPTLEDLNKYKEFLRMTESSSTEVLDS 68
QY 61 TVKDAVGTSVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
DB 69 TTKDVIQKGISVVGDLGVGVPPFGALVSFYTNFLNTIWPSE-DPWKAFMEQVEALMDQ 127
QY 121 KIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKSQDRIRLEFSAESHPFN 180
DB 128 KIADYAKNKALAEQLQGNVEDYVSALSSWKQNPVSSRNPHSQGRIRLEFSAESHPFN 187
QY 181 SMPSPAVSKFEVLFLPTTAAQANTHLLKDAQVGEWGYSSDVAEFYHRLKLTQOY 240
DB 188 SMPSPAISGYEVLFTTAAQANTHLLKDAQIYGEWGYEKEDIAEFYKRLKLTQOY 247
QY 241 TDHCVNWNVGLNGRGSTYDAWKVFNRRREMTLVLDLIVLPFYDIRLYSKGVKTEL 300
DB 248 TDHCVKWNVGLDKRGSSYEWVNFNRYRREMTLVLDLIALFPLYDRLVPKEVKTEL 307
QY 301 TRDIFTDPIFSLNTLOEYGPTELSENIRKPHLPDYLOQIEPHTRLQGYFGKDSFNW 360
DB 308 TRDVLTDPIVGNVNLRGYGTTFNENIRKPHLPDYLRHQHTFQGYGYGNDSPFNW 367
QY 361 SGNYVETRPSIGSSKTIITSPFYGNKSSPEVQNLFEENGKVVYRAVANTNLAVWPSA-VYSG 420
DB 368 SGNYVETRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKVVYRAVANTNLAVWPSA-VYSG 426
QY 421 VTKVDFSOYDDQKNSTQTYDSKRNHVSQAODSIDLPPETTDEPLEKAYSHQLNYAE 480
DB 427 VTKVEFSQYNDQDEASTQTYDSKRNHVSQAODSIDLPPETTDEPLEKAYSHQLNYAE 485
QY 481 CFLMQDRRGITPFTWTHRSVDFFNTIDAEKITQLPWRKAYALSASGASIIEGPGFGNML 540
DB 486 CFLMQDSRGITPVLWTHKSDVDFFNMIDSKKITQLPVRKAYLKQSGASVVAGRFRTGGDI 545
QY 541 LFLKESNSNTAKPKVTNLNSAALLQRYVRIRYASTNLRFLFVQNSNNDFLVLIYINTMKK 600
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546 IQCTE-NGSAATIVVT-PDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYVFDKTI 603
601 DDLITTYOTFDLATNNSMGFGSKNELIIGAESFVSNKEIYIDKIEPIV 650
604 GDTLTNTSNFNLASFSTPFELSG--NNLIQIGVTGLSAGDKVIYIDKIEPIV 651

RESULT 5
Q6PXN8 ID Q6PXN8 PRELIMINARY; PRT; 652 AA.
AC Q6PXN8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Insecticidal crystal protein.
GN Name=cry3;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]_TaxID=1428;
RP SEQUENCE FROM N.A.
RC STRAIN=YM-03;
RA Gao M., Cai Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY572010; AAS79487.1; -.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 652 AA; 74007 MW; AC2756FDED104A45 CRC64;

Query Match 68.6%; Score 2337.5; DB 2; Length 652;
Best Local Similarity 68.5%; Pred. No. 1.9e-144;
Matches 445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;

QY 1 MNPNNRSHDTIKVTNPSELQTNHNYPLADNPNSTLELNKYKEFLRMTESSSTEVLDS 60
DB 9 MNPNNRSHDTIKVTENNEVPTNHVQYPLAETPNPTLEDLNKYKEFLRMTESSSTEVLDS 68
QY 61 TVKDAVGTSVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
DB 69 TTKDVIQKGISVVGDLGVGVPPFGALVSFYTNFLNTIWPSE-DPWKAFMEQVEALMDQ 127
QY 121 KIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKSQDRIRLEFSAESHPFN 180
DB 128 KIADYAKNKALAEQLQGNVEDYVSALSSWKQNPVSSRNPHSQGRIRLEFSAESHPFN 187
QY 181 SMPSPAVSKFEVLFLPTTAAQANTHLLKDAQVGEWGYSSDVAEFYHRLKLTQOY 240
DB 188 SMPSPAISGYEVLFTTAAQANTHLLKDAQIYGEWGYEKEDIAEFYKRLKLTQOY 247
QY 241 TDHCVNWNVGLNGRGSTYDAWKVFNRRREMTLVLDLIVLPFYDIRLYSKGVKTEL 300
DB 248 TDHCVKWNVGLDKRGSSYEWVNFNRYRREMTLVLDLIALFPLYDRLVPKEVKTEL 307
QY 301 TRDIFTDPIFSLNTLOEYGPTELSENIRKPHLPDYLOQIEPHTRLQGYFGKDSFNW 360
DB 308 TRDVLTDPIVGNVNLRGYGTTFNENIRKPHLPDYLRHQHTFQGYGYGNDSPFNW 367
QY 361 SGNYVETRPSIGSSKTIITSPFYGNKSSPEVQNLFEENGKVVYRAVANTNLAVWPSA-VYSG 420
DB 368 SGNYVETRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKVVYRAVANTNLAVWPSA-VYSG 426
QY 421 VTKVDFSOYDDQKNSTQTYDSKRNHVSQAODSIDLPPETTDEPLEKAYSHQLNYAE 480
DB 427 VTKVEFSQYNDQDEASTQTYDSKRNHVSQAODSIDLPPETTDEPLEKAYSHQLNYAE 485
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Db 61 EVFLSEQDAVKAADIIVGKLLTGLGVFPVGPVLSLYTQILDILWFSKQSKQWEIWEQVE 120
Qy 116 VLIDKKIEYAKSALAELOGLONNFEDYVNALNSWKTPLSLRSKRQSDRIREFLSQAE 175
Db 121 ELINQKIAEYARNKALSEGLEGLNNYQLYLTAALEWKENPNSRALRD---VNRNFEILD 177
Qy 176 SHFRNSMPSFAVSKFEVLPLTYAQAANTHLLLLDKDAQVGEWGYSSDVAEFVHRQLK 235
Db 178 SLFTQMPSPFRVTFNEVPELTYTAAANLHLLLDASIFGEWGLSTSTINNYNRQWK 237
Qy 236 LTQQYTDHCVMWYVGLNGLRGSTYDAWKFNFRREMTLTVDLVLVLPFFDYDLISYKG 295
Db 238 LTAESVDCVKWYETGLAKLKSSAKQWIDYNQPREMTLTVDLVDVALFSNYDTTYPLA 297
Qy 296 VKTELTDRIDTDP-----IFSANTLOEQYGTPLFSIEN-SIRKPHLPDYLOQIEFHTRLOP 349
Db 298 TTAQLTREVTYDPLGAVDVPNIGSWYDKAPSFSEIEKAAIRPPHVEDYITGLTVYTKRS 357
Qy 350 GYFGKDSF-NYKSGNYVETRPISGSKTITSFPYGDKSTPEYQKLSFDGQKVYRTIANTD 408
Db 358 --FTSDRYMRYWAGHQISYK-HIGTSSTFTQMYGTQNLQSTSNFDFNYDIYKLTLSNGA 414
Qy 409 V---RAWPNKGVY--LGVTKVDFSOYDDQKNETSTQTYDSKRNNGHVSQAQSDIDOLPPE 463
Db 415 VLLDIVP-GYTYTFGMPETEYFVWNLNTRKLTLYPKASKDILDRTRDSELELPET 473
Qy 464 TDEPLEKAYSHQNYAECFLMQDRGTPTFPFTWTHRSVDFNTIDAETKITQLPVVKAVAL 523
Db 474 SQOPNYESYSHRLGHTFTYSSSTSYVDFVSWTHRSADLTNTVKSGETIQPGGKSSIT 533
Qy 524 SSGASIEGPGTGNLLFKESSNSIAKPKYTLNSAALLQRYRVRIRYAS--TTNLRLF 581
Db 534 GRNTYIIRKRGYTGDDVALTRIGS-CFQMFIPES---QRPRIRIRYASNETSYISLY 589
Qy 582 VQNSNN--DPLVIYINKTNKDDLTQYTFD-----LATTSNMGFSGDKNELIIGAES 633
Db 590 GLNQSGTLKFNQTSYNSKNEN---DLTYNDFKIEYPRVLSVNA---SSNIQRLSIGIQ- 641
Qy 634 FVSNEKIYI-DKIEFTIPV 650
Db 642 --TNTNLFILDRIEFTIPV 657
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RESULT 11

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C9CA_BACTO STANDARD; PRT; 1157 AA.
ID C9CA_BACTO
AC Q45733;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry9Ca (insecticidal delta-endotoxin
DE CryIXC(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry9Ca; Synonyms=cryIXC(a);
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1442;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=BTS02618A;
RX MEDLINE=96141404; PubMed=8572715;
RA Lambert B., Buysse L., Decock C., Janssens S., Piens C., Saey B.,
RA Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peferoen M.;
RT "A Bacillus thuringiensis insecticidal crystal protein with a high
RT activity against members of the family Noctuidae."
RL Appl. Environ. Microbiol. 62:80-86(1996).
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of Lepidoptera larvae. Has a fairly broad
CC spectrum of activity against members of the Pyralidae,
CC Plutellidae, Sphingidae and Noctuidae families. It was the first
CC insecticidal crystal protein characterized with activity against
CC cutworms. No activity is observed against some beetles, such as
```

```
CC the Colorado potato beetle.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; Z37527; CAA85764.1; -.
DR PIR; A59350; S49247.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF0555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Direct protein sequencing; Sporulation; Toxin.
KW SEQUENCE 1157 AA; 129775 MW; C364391EF7DFB8A CRC64;
SQ
Query Match 33.1%; Score 1127.5; DB 1; Length 1157;
Best Local Similarity 36.1%; Pred. No. 6.7e-65;
Matches 250; Conservative 148; Mismatches 217; Indels 77; Gaps 19;
Qy 1 MNPNNRSHDTIKVTPNSELOTNEN-QYPLADNPNTLEELNYKEFLRWTESSSTEVDLN 59
Db 1 MNRNNQNEYIID-APHGCFSDDDRYPLASDPNAAQLNMNYKYDQLQMTDEYTDYSYN 59
Qy 60 STV---KDVGTVGSVVGQILGVVVPFAGALTSFYQSFLNTIWP-SDADPWKAFMAQV 114
Db 60 PLSISGRDANVQATLTVVGRILGALGVFSPQISFYQFLNTLTPVNDTALWEAFMRQV 119
Qy 115 EVLIDKKIEYAKSALAELOGLONNFEDYVNALNSWKTPLSLRS-KRSQDRIREFLSQ 173
Db 120 EELVNNQITFEPARNQALRLQGLGDSFNVYQSLQNW---LADRNDTRNLSSVVAQFTA 175
Qy 174 AESHFRNSMPSFAVSKFEVLPLTYAQAANTHLLLLDKDAQVGEWGYSSDVAEFVHRQ 233
Db 176 LDLDFVNAIPLFAVNGQQVPLLSVYAQAVNLHLLLDKASLFGEGWGFTQGSISTYYDRQ 235
Qy 234 LKLTQYTDHCVMWYVGLNGLRGSTYDAWKFNFRREMTLTVDLVLVLPFFDYDIRLYS 293
Db 236 LELTAKYNYETWNTGLDRLGRTESWLRYHQFRREMTLVLDVVALFPYDVLVLP 295
Qy 294 KGVKTELTDRIDTDPF-----SLNLTQEQYGP---TFLSIENS-IRKPHLPDYLOQIEF 343
Db 296 TGSNFPQLTREVTYDPIFVNPPANVGLCRRWGTNPYNTFSELENATIRPPLFDRLNSLTI 355
Qy 344 HTRLOPGYFGKDSFNYWSGNYVETRPISGSKTITSPEY-----GDKSTPEVQ 391
Db 356 SSNREF--VSSNFMDFWSGHTL--RRSYLNDLSAQQEDSYGLITTTTATINPGVDGNRIE 411
Qy 393 KLSFDGQKVYRTIANTDVAWPNKGVYLVTKVDFSOYDDQKNETSTQTYDSKRNNGHVS 451
Db 412 STAVDFRSGALIGYVNRASFPVGGFLNGTT-----SPANGGCRD 451
Qy 452 AQDSIDQLPPEPTTDEPLEKAYSHQNYAECFLMQDRR-----GTIPFTWTHRSVDPF 504
Db 452 LYDNTDELPPDBS----TGSSTHRLSHVTFESFQTNQAGSIANAGSVPTVYVWTRRDVDLN 507
Qy 505 NTIDAETKITQLPVVKAVALSGASIEGPGTGNLLFKESSNSIAKPKYTLNSAALQ 564
Db 508 NTITPNRITQLPLVKASAPVSGTTLKPGPGFTGGGILL-RRITNGTFTGLURVTVNS-PLTQ 565
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CC -----
DR HMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1229 AA; 139769 MW; AAC949DB675C3269 CRC64;

Query Match 32.9%; Score 1122; DB 1; Length 1229;
Best Local Similarity 36.7%; Pred. No. 1.7e-64;
Matches 247; Conservative 126; Mismatches 248; Indels 52; Gaps 16;

QY 1 MNPNNRSHDTIKVTPNSELOTHNQYPLADNPSTLEELNYKEFLRMTEDS----STEV 56
DB 1 MTSNRKNEI-----NALSIPTVSNPST---QMNLSPDARI-EDSLCVAEVNN 46

QY 57 LDNSTVKDVGTSVVGQILGVGVPPFAGALTSPYQSFNTIMPSPDADPWKAFMAQVEV 116
DB 47 IDPFVSASTVQTGINAGRIILGVLPFAGLASFSYFLVGLWPSGRDPWEIFLEHVEQ 106

QY 117 LIDKKEEYAKKALAEQLQNNFEDYVNALNSWKTPLSLRKSRQDRIRLEFSQAES 176
DB 107 LIRQVQVTRNTARLEGLRGYRSYQOALETWLD---NRNDARSIIILERYVALEL 163

QY 177 HFRNSMPFAVSKFEVLFLPTVYQAANTHLLLLKDAQVFGEEWGSSEDAVFYHRQLKL 236
DB 164 DITTAIPLRIRNEEVPLLMVYQAANLHLLLRDASLFGSEWGSMASSDVNQYQEQIRY 223

QY 237 TQOYTDHCNVNVLNGLRGSTYDAWKFNFRREMTLTVDLIVLFFYDIRLYSKGV 296
DB 224 TEEYSNHCQVQWYNTGLNNLRGTNAESWLRYNQPRDLTLGLVDLVALFPSTYDTRYPINT 283

QY 297 KTELTRDITDPI-----PSLNTLQEYGTFLSIENSI-RKPHLFDYLQGLEFHR 346
DB 284 SAQLTREIYTDPIGRTNAPSGFASFWNNAPSFAIAEALFRPHLLDFFPEQLTIYS- 342

QY 347 LQPGYFGKDSFNWGSNGYVETRPISGSKTITSPFYGDKSTBPVQKLSFDGQKVRTIAN 406
DB 343 ASSRWSSSTQHMNVVGHRLNFRPIGTLNTSTOGLTNNTSINPV-TLQFTSRDVRVTESN 401

QY 407 TDVAAMPNGKYLGVTKVD-----FSQVDDQK-NETSTQYDSKRNKHGVSAQDSIDOL 459
DB 402 A-----GTNILFTTPVNGVPWARENFINPQNIYERGATTYSQYQGVIGLFDSETEL 454

QY 460 PPETTDEPLEKAYSHOLNVAECFLMDQRCGTIPFTWTHRSVDFFNTIDAEKITQLPVVK 519
DB 455 PPETTERPNYESHRLSHLIGLIGNTLRA--PVSWTHRSADRTWIIGNRITQIPLVK 512

QY 520 AYALSSGASIIIEGPGFTGGNLLFLKBSNSIAKFKVTLNSAALLQRYRVRIRYASTNNLR 579
DB 513 ALNLHSGVTVVGPGFTGGDIL-RRNTGTGFGDIRNLN-VPLSQRYRVRIRYASTTDLQ 570

QY 580 LFVQNSNDFLVIYINKTMKDDLLTYQTFDPLATNSNMGFGSKNELIIGAESFVSNEK 639
DB 571 FFRINGTNTNIGNFSRTNRGNLEYSRFTAGFTPTPFNFLNAQSTFTFLGAQSP-SNOE 629

QY 640 IYDKIEFIPVOL 652
DB 630 VYIDRVEFVPAEV 642
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RESULT 14

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CLBC_BACTM STANDARD; PRT; 1233 AA.
ID AC Q45774;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin
DE CryIbC) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbC; Synonyms=cryIb(C), cryIb;
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RA Bishop A.H., Bone E.J., Ellar D.J.;
RT "Cloning of novel Bacillus thuringiensis delta-endotoxin.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR HMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 32.9%; Score 1122; DB 1; Length 1233;
Best Local Similarity 36.7%; Pred. No. 1.7e-64;
Matches 247; Conservative 126; Mismatches 248; Indels 52; Gaps 16;

QY 1 MNPNNRSHDTIKVTPNSELOTHNQYPLADNPSTLEELNYKEFLRMTEDS----STEV 56
DB 1 MTSNRKNEI-----NALSIPTVSNPST---QMNLSPDARI-EDSLCVAEVNN 46

QY 57 LDNSTVKDVGTSVVGQILGVGVPPFAGALTSPYQSFNTIMPSPDADPWKAFMAQVEV 116
DB 47 IDPFVSASTVQTGINAGRIILGVLPFAGLASFSYFLVGLWPSGRDPWEIFLEHVEQ 106

QY 117 LIDKKEEYAKKALAEQLQNNFEDYVNALNSWKTPLSLRKSRQDRIRLEFSQAES 176
DB 107 LIRQVQVTRNTARLEGLRGYRSYQOALETWLD---NRNDARSIIILERYVALEL 163

QY 177 HFRNSMPFAVSKFEVLFLPTVYQAANTHLLLLKDAQVFGEEWGSSEDAVFYHRQLKL 236
DB 164 DITTAIPLRIRNEEVPLLMVYQAANLHLLLRDASLFGSEWGSMASSDVNQYQEQIRY 223

QY 237 TQOYTDHCNVNVLNGLRGSTYDAWKFNFRREMTLTVDLIVLFFYDIRLYSKGV 296
DB 224 TEEYSNHCQVQWYNTGLNNLRGTNAESWLRYNQPRDLTLGLVDLVALFPSTYDTRYPINT 283

QY 297 KTELTRDITDPI-----PSLNTLQEYGTFLSIENSI-RKPHLFDYLQGLEFHR 346
DB 284 SAQLTREIYTDPIGRTNAPSGFASFWNNAPSFAIAEALFRPHLLDFFPEQLTIYS- 342
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QY 347 LQPGYFGKDSFNWYSGNYVETRPISGSKTITSPFYGDKSTPEYQKLSFDGQKVYRTIAN 406
D 343 ASSRWSSTQHMNVYVGHRLNFRPIGGTLTSTQGLTWNNTSINPV-TLOFTSRDYRTESN 401
QY 407 TDVAWPNKGYLVGTQVD-----FSQYDDQK-NETSTQYDSKRNGHVSQAQSDQL 459
D 402 A-----GTNLTPTVGVGPWFARFNPQNIYERGATTSYQPYQGVGQLPDSSETL 454
QY 460 PPETTDPLEKAYSHQNLNVAECFLMQDBRGITPEFTWTHRSVDFFNTIDAEEKITOLPVVK 519
D 455 PPETTERPNYESYSHRUSHGLIIGNTLRA--PVYSWTHRSADRTNTIGNRITQIPLVK 512
QY 520 AYALSSGASIEGPGFTGGNLLFLKSSNSTAKPKVTLSAALLQRYRVRIRVASTTNLR 579
D 513 ALNLHSGVTVVGGPGFTGGDIL-RRNTGTGFDRLNIN-VPLSQRYRVRIRVASTIDLQ 570
QY 580 LFVQNSNDELVIYINKTMKDDDLTYQTDLDATTNSMFGSGDKNELIIGASFSVNEK 639
D 571 FFRINGTTNIGNFSRTMRGDLNLEYSFRSTGFTSPFNFLNAQSTFTLGAQSF-SNOE 629
QY 640 IYIDKIEFIPVOL 652
D 630 VIIDRVSEFPAEV 642

RESULT 15
C1KA_BACTM STANDARD; PRT; 1215 AA.
ID C1KA_BACTM STANDARD; PRT; 1215 AA.
AC Q45715;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cry1Ka (Insecticidal delta-endotoxin
DE Cry1Ka(a)) (Crystalline entomocidal protoxin) (137 kDa crystal protein).
GN Name=cry1Ka; Synonyms=cry1K, cry1K(a);
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FI90;
RX MEDLINE=96102856; PubMed=9586263; DOI=10.1016/0378-1097(95)00397-1;
RA Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
RT "Cloning of a novel crystal protein gene cry1K from Bacillus
RT thuringiensis subsp. morrisoni".
RL FEMS Microbiol. Lett. 134:159-164(1995).
CC -I- FUNCTION: Promotes colloidotomotic lysis by binding to the midgut
CC epithelial cells of insects. Selectively toxic to Artogetia rapae
CC but not active on Plutella xylostella.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1215 AA; 137378 MW; 7CAF7A3311893D9B CRC64;

Query Match 32.9%; Score 1121; DB 1; Length 1215;
Best Local Similarity 37.9%; Pred. No. 1.9e-64;
Matches 251; Conservative 126; Mismatches 247; Indels 38; Gaps 16;

QY 1 MNPNNSEHDTIKVTNSELQTNHNOYPLADNPNSTLEELNYKEFLRMSTDSSTEVLDNS 60
D 1 MNSNRKNNEIINALIPAVNSHAQMDL--SPDARIE-----DSCVAEGNN---IDPF 50
QY 61 TVDADVGTGIVSVVQGLVGVVPFAGALTFSYQSELTNIWPSDADPWKAPMAOVVLI-D 119
D 51 VSASTVQTGSIAGRIILGVLPFAGALASFSYFLVGLWPSGRDPWEIMEHVEQIVRQ 110
QY 120 KKTIEEVAKSALAELOGLQNNFEDYNALNSWKKTPLSLRSKRQSDRIIRLFQSAESHFR 179
D 111 QQTITDSVRDTAIARLEGLGRGYSYQQALETWLD--NRNDARSRSIIRERYIALELDIT 167
QY 180 NSMPSFAVSKFEVLELPTVAAQAAANTHLLLLKDAQVGEEMGYSSYEDVAEYFHRQLKLTQ 239
D 168 TALPLFSIRNEEVPLLMVTAAANLHLLLDASLFGSEWMSADVNYIQOIRITEE 227
QY 240 YTDHCYNNVNGVLNGLRGSTYDAWKFNRRPREMTLTVDLIIVLFPFYDIRLSKGVKTE 299
D 228 YSNHCYQVYNTGLNRLRGTTAETWRYNQFRDLTLGLVDLVALFPSYDTRTYPITTAQ 287
QY 300 LTRDIFTDPIFSL-----NTLOEYGPFLFSIENS-IRKPHLFYDLOGIEFHTRLQPVFGK 354
D 288 LTRREVYTDPNVGVAGPNNSWFRNGASFSAIENAIIRQPHLYDFLTNLTIVTR--RSQVGT 345
QY 355 DSFNYSYGNVVERPISGSKTITSPFYGDKSTPE--VQKLSFGQKQVYRTIANQDVAAM 412
D 346 TINLWAGHRITNRIQGG--TSEWVGAIINPVSDIPFNVRDVRVTVSLAGGLGS 402
QY 413 PNGKVLGVTKVDQFQYDDQKNETSTQTYDSKKNNGH---VSAQDSIDOLPPTTDEPL 468
D 403 LSGIRY-GLTRVDVDFMIRNHPDIVTGLF---YHPGHAGIATQVKDSDELPLETTEQPN 458
QY 469 EKAYSHQNLNVAECFLMQDBRGITPEFTWTHRSVDFFNTIDAEEKITOLPVVKALVSSGAS 528
D 459 YRAFSPHLLSHIS--MGFTTQDVPVYVSWTHQSADRTNTINSRITQIPLVKAHTLOSGETT 516
QY 529 IIEGPGFTGGNLLFLKSSNSTAKPKVTLSAALLQRYRVRIRVASTTNLRVQNSNND 588
D 517 VVKGPGFTGGDIL-RRTSGGPFAPFSNVNLD-FNLSQRYRVRIRVASTTNLRIVTVVAGER 574
QY 589 FLVIYINKTMKDDDLTYQTDLDATTNSMFGSKNELIIGAESFVSNKIIYDKIEFI 648
D 575 IFAGQFDKTMADAGAPLTFQSFVATINTAFTFPERSSSLTIGADTFSSNGNEVVDREFELI 634
QY 649 PV 650
D 635 QV 636

RESULT 16
C7AA_BACTU STANDARD; PRT; 1138 AA.
ID C7AA_BACTU STANDARD; PRT; 1138 AA.
AC Q03749;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry7Aa (Insecticidal delta-endotoxin
DE CryVIIA(a)) (Crystalline entomocidal protoxin) (129 kDa crystal
DE protein).
GN Name=cry7Aa; Synonyms=cryIIic, cryVIIA(a);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=92384571; PubMed=1514800;
RA Lambert B, Hofte H., Annys K., Janssens S., Soetaert P., Peferoen M.;
RT "Novel Bacillus thuringiensis insecticidal crystal protein with a
RL silent activity against coleopterian larvae.";
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of Coleoptera. This protein is not toxic in its
CC natural form. It is highly toxic to Colorado potato beetle larvae
CC after an in vitro solubilization and trypsin activation step.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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CC -----
DR EMBL; M64478; AAA22351.1; -.
DR EMBL; A07236; CAA00646.1; -.
DR PIR; A48944; A48944.
DR HSSP; P07130; 1DLCL.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Spolulation; Toxin.
DR KW SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;
SQ
Query Match 32.9%; Score 1119; DB 1; Length 1138;
Best Local Similarity 36.8%; Pred. No. 2.4e-64;
Matches 251; Conservative 120; Mismatches 237; Indels 74; Gaps 19;
QY 1 MNPNNRSEHTIKVTNSELQTHNQVPLADNPNSTLEELNYKEFLRMTEDSSSTEVLDS 60
DB 1 MNLNLLGDYSDSNTLNLSL-----NYPTQKALSPSLKMNWQDFLSITREQPEALASG 55
QY 61 TVKDAVGTGIVSVGQIILGVGVFPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
DB -AINTVSVTGATLSALGVGASFTITNFKIAGLLWPENGKIWDEFMTVEALIDQ 113
QY 121 KIEEYAKSALAELOGLQNNFEDYVNALNSW---KKTPLSLRKRQDRIRLFSAESH 177
DB 114 KIEEYVKNKATAELDGLGSALDKYQKALADWLKGQDDPEALISVATEFRI-----IDSL 167
QY 178 FRNSMPSFAVSKFVFLPFTVYQAQANTHLLLLKDAQVFGEEGWYSSDVAEFYHRQLKT 237
DB 168 FEFMSPFKVTGIEPILTVYQAQANHLALLRDSITLYGKWGFTQNNIEENYRQKRI 227
QY 238 QOYTDHCNNVYNGLNGRSTYDAWKNFRFRMTLTVLDLVLPPFDIILYSKGVK 297
DB 228 SEYSDHCTKWNSGLSLRNGSTYEQWYNFRFRMTLMDLVAVFPFDPDRRSMETS 287
QY 298 TELTRDITFDIPSLNTLOEGPTFLSTEN-SIRKPHLFYVLOGIEPHT-----RLQ 348
DB 288 TQLTREVTDDVSLUSISNPDIGPSQONETALTPHLVDLYLITYTSKYKAFSHEIQ 347
QY 349 PGYFGKDSFNWGSNGYVETREPSIGSKTITSPPFYGDKSTBPVKQ--LSFDGQKYRTIAN 406
DB 348 PDLF-----YWSAHKVSFKKS-EQSNLYTTGIYG-KTSGVSSGAYSFHGNDIYRTLAA 399
QY 407 TDVAAMPNGKYLGVTKVDFQYDQKNETSTQYDSEKNGNHVSADSDIDQLPPETTD 466
DB 400 PSVVVYPTQNY-GVEQVEFYGVKGHVHYRGDNKYD-----LTYDSIDQLPDP--GE 448

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QY 467 PLEKAYSHOINVAECFLMOD---RRCTIPFTWTHRSVDFPENTIDAEKITOLPVVKAYAL 523
DB 449 PIHEKYTHRLCHATAIFKSTPDYDNATIPFISWTHRSABYIYNNRIYPNKTIKIPAVKMYKL 508
QY 524 SSASIIIEGPGFTGNNLLFLKSSNSIAKPKVTLNSAALLQRYVRIRYASTTNLFLVQ 583
DB 509 DDPSTVVGKPGFTGGDLV-KRGSTGVIGIKATVNS-PLSQKVRVRVYAT-----557
QY 584 NSNDFLVYIN-----KTMKDDDLTYQTFDLATTNSNMGFGSGDKNELIIG 630
DB 558 NVSGQENV-YINDKITLQTKFQNTVETIGEGKDLTYGSEFYIYESTTIQFPDHPKHTLH 616
QY 631 AESFVSNKIYIDKIEFIPVOL 652
DB 617 LSDLSNNSSFYVDSIEFIPVDV 638
RESULT 17
Q9F0P8 PRELIMINARY; PRT; 719 AA.
AC Q9F0P8; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CrvII.
GN Name=crvII;
OS Bacillus thuringiensis.
OC Plasmid pBTC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX MEDLINE=22837682; PubMed=12957903;
RX DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
RA Hu Y., Li G., Huang D.;
RT "Identification of crvII-type genes from Bacillus thuringiensis
RT strains and characterization of a novel crvII-type gene.";
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
DR KW SEQUENCE 719 AA; 81024 MW; 7E17481922C435B6 CRC64;
SQ
Query Match 32.8%; Score 1118.5; DB 2; Length 719;
Best Local Similarity 37.3%; Pred. No. 1.3e-64;
Matches 253; Conservative 130; Mismatches 235; Indels 61; Gaps 17;
QY 1 MNPNNRSEHTIKVTNSELQTHNQVPLADNPNSTLEELNYKEFLRMTEDSS 53
DB 1 MKLKMPDKHQSSNAKVKDKIATDS-----LKNETDIELKNINHEDFLRMSHES 50
QY 54 TEVLNPNSTVKDAGTGISVVGQILGVGVFPFAGALTSFYQSFLNTIWPSDADPWKAFMAQ 113
DB -IDPFVSASTIQTGIGIAGKILGTGVPFAGIASLYSFTILGELWPKGSKQWEIFMEH 107
QY 114 VEVLIDKKEEYAKSALAELOGLQNNFEDYVNALNSMKTPLSLRKRQDRIRLFESQ 173
DB 108 VEELIDQKISTYARNIALADLKGDLALAVYHESLESWK---NRRNARATSVVKSQYIA 164
QY 174 AESHPNPSMPSFAVSKFVFLPFTVYQAQANTHLLLLKDAQVFGEEGWYSSDVAEFYHRQ 233

```

Db 165 LELLFVQKLSFAVSGSEVPLLPITYAQAANLHLLLRDASVFGKEMGLSNQISTFYNRQ 224
Qy 234 LKLTQOYTDHCVMWYVGLNGLRSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYS 293
Db 225 VERTSDYSDHCVMWYVGLNGLRSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYS 284
Qy 294 KGVKTELTRIDFDPISLNTLOBY-----GPTFLSIENS-IRKPHLFYDLOGIEF 343
Db 285 IKTSQLTREYVYDAICTVHPNASFATWYNNAPSFSAIESAVVRNPHLLDFLEQVTI 344
Qy 344 HTRLQPOYFGKDSFNWYVGLNGLRSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYS 403
Db 345 YSLLS-RWSNTQYNNMGHRLFR-TIGGVLTNTSGTNTSINPV-TLPFTSRDYRT 401
Qy 404 IANTDVAAPNGKYLGVTKVDSQYDDQKNESTQYDYSKRNNGHVA-----QDSIDLQ 459
Db 402 ESLAGLMLFQPNV-GVPRVDF-----HWKPAFLPIASDFFYLYGVAGVTQLODSENE 456
Qy 460 PPETTDPELEKAYSHQNLNAYAECLFMQDRRGITPFFTWTHRSVDFPNTIDAEKITQLPVVK 519
Db 457 PPETGQPNYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTEIENSITQPLVK 514
Qy 520 AYALSGASIIIEGPGFGGNNLLFKESSNSIAKPKVTLSAALLQRYVRIRYASTNLR 579
Db 515 AFNLSSGAAVRGPFGTGGDIL-RRNTGTGFGDIRVNN-PPFAQRYVRIRYASTNLR 572
Qy 580 LFVQ-----NSNDFLVIYINKTKDDLTQTPDLATNSMFGSGDKNELIIGAES 633
Db 573 FHTSINKALNQG-----FSATMNRGEDLYKTFTVGTFTFPFSGFQSTFTIGAWN 626
Qy 634 FVSNKIIYIDKIEFIPVOL 652
Db 627 FSSGNEVYIDRIEFVPEV 645

RESULT 18

C7AB_BACUC STANDARD; PRT; 1138 AA.
AC 045708;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry7AB (Insecticidal delta-endotoxin
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein)
GN Name=cry7AB; Synonyms=cryVIIA(b);
OS Bacillus thuringiensis (subsp. *kumamotoensis*).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD867;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch.

CC EMBL; U04368; AAA21121.1; --
DR HSP; P07130; 1DLG.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1138 AA; 129658 MW; E12DC80COA56D1DA CRC64;
Query Match 32.8%; Score 1117; DB 1; Length 1138;
Best Local Similarity 37.2%; Pred. No. 3.2e-64;
Matches 253; Conservative 115; Mismatches 242; Indels 70; Gaps 19;
Qy 1 MPNNRSEBDTIKVTNSELQTNHNYPLADNPSTLEELNYKEFLRMTESSSTEVLNLS 60
Db 1 MLNLNLGVEDSNRTLNLSL-----NYPQKALSPSLKNNYQDFLSITEREQPEALASG 55
Qy 61 TVKDAVGTGIVGVQILGVVGPFGALTSFYQSPLNTIWPSSADPWKAPMAQVEVLIDK 120
Db 56 NT--AINTVSVTGATLSALGVFGASFITNFYLIKITGLLWPHDKNIWDEFMTEVETLIEQ 113
Qy 121 KIEYAKSKALAELOGLQNNFEDYVVALNSWKTPLSRSKRSQDRIELPFSQASHFRN 180
Db 114 KIEQYARNKALAELEGNNLTYYQALLEDWLNPP--DDPATITRVIDRFRILDALFES 170
Qy 181 SMPFAVSFVELFLPTAQAANTHLLLLKDAQVGEEMGYSSSEDVAEFYHRLKLTQY 240
Db 171 YNPSFRVAGVEIPLLTVYAQAANLHLLLRDASVFGKEMGLSNQISTFYNRQ 230
Qy 241 TDHCVMWYVGLNGLRSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYSKGVKTEL 300
Db 231 SNHCVMWYVGLNGLRSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYSKGVKTEL 290
Qy 301 TRDIFTDPIFSLNTLOBYGPTFLSIENS-SIRKPHLFYDLOGIEFHT-----RLQPGY 351
Db 291 TREVTDPISLSISNPGIGSFSQMENTAIRTHLVLDYLDLYIYSKYKAFSHEIQPDL 350
Qy 352 FGKDSFNWYVGLNGLRSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYSKGVKTEL 409
Db 351 F-----YNSAHKVPKQS-EQSNLYTTGIYG-KTSGYSSGAYSFRGNDIYRTLAAPSV 402
Qy 410 AAWPNCKYVLGVTKVDSQYDDQKNESTQYDYSKRNNGHVAQDSIDQLPPTTDEPLE 469
Db 403 VVYPTQNTY-GVEQVEFYGVKGHVHVRGDNKYD-----LTYDSIDQLPPD--GSEPIH 451
Qy 470 KAYSHOLNAYAECLFMQD--RRGTIPFFTWTHRSVDFPNTIDAEKITQLPVPKAYALSSG 526
Db 452 EKXTHRLCHATAISKSTPDYDNATIPFSWTHRSAYEYRIYENKIKITPAVKMYKLGDT 511
Qy 527 ASIIEGPGFGGNNLLFKESSNS-IAKPKVTLSAALLQRYVRIRYASTNLRFLVQNS 585
Db 512 STWVGPGFTGGDL--VKGSGNGYIGDIKATVNS-FLSQNYRVRVRYAT-----NV 559
Qy 586 NNDFLVIYN-----KTNKDDLTQYTFDLATNSMFGSGDKNELIIGAE 632
Db 560 SQGFNY-YINDKITLQRKFQNTVETIGEGKDLTGYSGFYEVSTTIQFPDKPKITLHLS 618
Qy 633 SFVSNKIIYIDKIEFIPVOL 652
Db 619 DLSNNSFFVDSIEFIPVDV 638

RESULT 19

C11D_BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Pesticidal crystal protein cryII(d) (Insecticidal delta-endotoxin)
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryII(d); Synonyms=cryII(d), NRcryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RA MEDLINE=20374042; PubMed=10919402;
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
gene.";
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae. Active on Plutella
CC xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF047579; AD44366.1; -.
DR HSSP; P02965; 1C1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 32.8%; Score 1115.5; DB 1; Length 719;
Best Local Similarity 37.8%; Pred. No. 2.1e-64;
Matches 253; Conservative 123; Mismatches 225; Indels 69; Gaps 18;

QY 23 NHQY-----PLADNPSTLEELNYKEFLRMTEDSSTE-VLDNSTVKDAV 66
DB 5 NQNYRFSFNATVDKSFDTDPLEHNTNMEQLQNSHEDCLKMSEYSEVFPVSVSTIQ--- 61

QY 67 GTGISVVGQILGVVFPFAGALTSTFQSFINTWPSDADPWKAFMAQVEVLDDKIEEYA 126
DB 62 -TGIGIAGKILGNLGVFPFAGQVASYLFIILGELWPKGQWELFMEHVELINQKISTYA 120

QY 127 KSAIAELQGLQNNFEDYNALNSWKKTPLSLSEKSDRIREL-----FSQAESHPNSM 182
DB 121 RNKALADLKLGLDALAVYHESLESWE-----NRNTRVRSVKNQVIALELMFVQKL 173

QY 183 PSFAVSKFEVFLFTYAQAANTHLLLLKDAQVGEWGYSSSDVAFYHRQLKLTQOYTD 242
DB 174 PSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSESEISFTYNRQSSQTQYSD 233

QY 243 HCWNVTNVLNGLRGSTYDAWVFNFRREMTITVLDDLVLFPFYDIRLSKGVKTELTR 302
DB 234 YCSEWYNTGLNRLGTNAESWRYNQPRDMTLWLDLVALFSPYDTRMYPDPTSQLTR 293

QY 303 DIFTDPFISLNTLQY-----GPTFLSIENS-IRKPHLDYLLQGIIEFFRLQPGYF 352
DB 294 EVYTDALGTVHPNASFASTWYNNNAPSFTIEAAVRNPHLLDFLEQVITYLLS-RWS 352

QY 353 GKDSFNWMSNGYVETRPISGSKSTITSPPFYGDKSTEPVQKLSFDGQKVRVTIANTVAW 412

DB 353 NTQVMNMGHGKLEFR-TIGTLNLTSTQGSTNTSINPV-TLPFTSRDVYRTESLAGLNLF 410
QY 413 PNGKVLGVTKVDFSQYDDOKNETSTQTYDSKRNHG-----VSAQDSIDOLPPTTDEPL 468
DB 411 LTQPVN-GVPRVDF---HWKFVTHPIASDNFYVPGYAGIGTQLQDSENELEPPTTQPN 465
QY 469 EKAYSHOLNVAECFLMQDRRGTIPTFFTWTHRSVDFNTIDAETITQLPVVKAYALSSGAS 528
DB 466 YESYSHRLSHIGLISASHVALV--YSWTHRSADRTNTINSDSITQPLVKAFNLPASGAS 523
QY 529 IIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQRYRVIRYASTTNRLFLVQ----- 583
DB 524 VWRGPGFTGDDIL-ORTNTGTGDIRVNIN-PFPAQRYRLRIRYASTTNLEFFHTSINGKA 581
QY 584 -NSNDFELVIYINKTKNDDDLTQTQFDLATTNSMGFSGDKNELLIIGASFVSNEKIYI 642
DB 582 INQGN-----FSATMNRGDLDYKAPRTVGTFTTFFSNAQSTFTTIGAWNFSLGNEVIYI 635
QY 643 DKIEFIPVOL 652
DB 636 DRIEFVPEV 645

RESULT 20
C7AB_BACUA
ID C7AB_BACUA STANDARD; PRT; 1138 AA.
AC Q45707;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry7Ab (Insecticidal delta-endotoxin
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry7Ab; Synonyms=cryVIIA(b);
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD511;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active toxins";
RT coleopteran-active toxins.";
RL Patent number US5286486, 15-FEB-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U04367; AAA21120.1; -.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;

Query Match 32.6%; Score 1112; DB 1; Length 1138;
Best Local Similarity 36.8%; Pred. No. 6.8e-64;
Matches 248; Conservative 124; Mismatches 244; Indels 58; Gaps 19;

Qy 1 MNPNNRSEHTIKVTPNSELQTNHNPQLADNPNTLLEELNYKEFLRMWDSSTFVLDNS 60
Db 1 MNLNLGGYEDSNRLNLSL-----NYPTKALSPSLKNMNYQDFLGITEREQPEALASG 55
Qy 61 TVKDAVGTGIVSGQILGWGVRPAGALTSFYQSFLNTIMPSDADPKAFMAQVEVLIDK 120
Db 56 NT--AINTVSVTGATLSALGVPAGSFTITPFLKITGLWPHNKNINWDEFWTEVETLIEQ 113
Qy 121 KIEEYAKSKALAEQLQGNPFEDVYNALNSWKKTPLSLRSKRSQDRIRSELFQSAEHSFRN 180
Db 114 KIEGYARNKALAELEGLGNLTIYQQALEDWLNPP---DOPATITRVIDFRILDALFES 170
Qy 181 SMPFSAVSKFEVLEPLPYAQANHTHLLLDKQAVFGBEWGSVDVAEFYHRQKLTQQY 240
Db 171 YMPFSRVAGYEIPLLTYYAQANHLALLRDLSTLYGDKWGTQNNIEENTNRQKKHISEY 230
Qy 241 TDHCVNMYNGLNGRSTYDAWKENRFRREMTLVLDLVLVLPFFYDIRLYSKGVKTEL 300
Db 231 SNHCVKYNGSLRNGSTTEQWYNRFRREMILMVDIAAVPEIYDPRMYSMETSTQL 290
Qy 301 TRDIFTDPIFSLNTLOEYGPTEFLSIEN-SIRKPHLFYLOQIEPHT-----RLQPGY 351
Db 291 TREVYTDPISLISNPIDGSPFSQMENTAFRPHLDVLDLDELYITSKYKAFSHEIQPDL 350
Qy 352 FGKDSFNWNGVNGVETRPSIGSSKTTISPPYGDKSTEPVOK--LSFGQKQYRTIANTDV 409
Db 351 F-----YWCVHKVSPFKS-EQSNLYTTGIYG-KTSGYISSGAYSPRGNDIYRTLAAPSV 402
Qy 410 AAMPNGKVLGVTKVDFSDYDDQKNSTSTQYDSKRNNGHVSAQDSIDQLPPTTDEPLE 469
Db 403 VVPYPTONY-GVEQVEFYGVKGVHYRGDNKYD-----LTYDSDDQLPDP--GSPIH 451
Qy 470 KAYSHQNLNVAECFLMQD---RRGIPFPTTHRSVDFFNTIDAEKITPLPWKAYALSSG 526
Db 452 EKYTHRLCHATAISKSPDYDNATIPFSTHRSAYEYNYRPNKIKIIPAVKXKLDL 511
Qy 527 ASIEGPGFTGNNLLFLKESNS-IAFKVTVLSAALLQYRVIRVASTTN--LRLFVQ 583
Db 512 STVVGFGFTGGDL--VKRSGNGYIGDIKATVNS-PLSKYQYRVRYVATSVGLFNVI- 567
Qy 584 NSNNDLVIYIN-----KTNKKDDLLTYQTFDLATNSNGFSGDKNELIIGAESFVNS 638
Db 568 ---NDEALQKQFQSTVETIGEGKDLTYGSGFYEVSTTIQFPNEHPKITLHLNLSNNS 624
Qy 639 KIYIDKIEFIPVQL 652
Db 625 PFYVDSIEFIPVDV 638

RESULT 21
C11A_BACTK
ID C11A_BACTK STANDARD: PRT: 719 AA.
AC Q45752; P71092; Q45750; Q45751; Q45756;
DT 30-MAY-2000 (Rel. 39, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Pesticidal crystal protein cryIIA (Insecticidal delta-endotoxin
DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Names-cryIIa; Synonym-SCGCRYV, cryII(a), cryV, cryV1;
OC Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSIR732;
RX MEDLINE=93298009; PubMed=8517758;
RA Gleave A.P., Williams R., Hedges R.J.;
RT "Screening by polymerase chain reaction of Bacillus thuringiensis

serotypes for the presence of cryV-like insecticidal protein genes and
characterization of a cryV gene cloned from B. thuringiensis subsp.
kurstaki.";
Appl. Environ. Microbiol. 59:1683-1687(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=JHCC4835;
RX MEDLINE=92269582; PubMed=1588820;
RA Taylor R., Tippet J., Gibb G., Pella S., Pike D., Jordan L., Ely S.;
RT "Identification and characterization of a novel Bacillus thuringiensis
delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";
Mol. Microbiol. 6:1211-1217(1992).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
thuringiensis and cloning of cryV-type genes from Bacillus
thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
entomocidus.";
Appl. Environ. Microbiol. 61:2402-2407(1995).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=AB88;
RX MEDLINE=96178985; PubMed=8606196;
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
Craig J.A., Kozel M.G., Estruch J.J.;
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus
thuringiensis: the cryV-encoded protein is expressed early in
stationary phase.";
J. Bacteriol. 178:2141-2144(1996).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=61;
RX Selvapandian A., Bhatnagar R.K.;
RT "Isolation, cloning and expression of cryV gene.";
Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
-I- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella and Bombyx mori.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; M98544; AAA22354.1; -
CC EMBL; X62821; CAA44633.1; -
CC EMBL; L36338; AAC36999.1; -
CC EMBL; L49391; AAB00958.1; -
CC EMBL; Y08920; CAA70124.1; -
CC PIR; I39815; I39815.
CC PIR; S25383; S25383.
CC HSSP; P02965; IC1Y.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
VARIANT 159 K -> R (in strain 61).

05-JUL-2004 (TREMBlrel. 27, Created)
05-JUL-2004 (TREMBlrel. 27, Last sequence update)
05-JUL-2004 (TREMBlrel. 27, Last annotation update)
CryI.

OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
[1]

SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; --
DR GO: 0005102; Fireceptor binding; IEA.
DR GO: 0006952; P: defense response; IEA.
DR GO: 0009405; P: pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 32.3%; Score 1100.5; DB 2; Length 719;
Best Local Similarity 36.3%; Pred. No. 28-63;
Matches 249; Conservative 137; Mismatches 231; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTENSELQNNHNYPLADNPSTLEELANKFELRMTESS 53
DB 1 MKLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKMEYEN 50

QY 54 TE-VLDNSTVKDAVGTGIVGQILGVGPAGALTSFYQSFLNTIWPSDADPWKAFMA 112
DB 51 VEPFVSASTIQ---TGIGIAGKILGTGVGPAGQVASYLSFILGELAPKGNQWEIEME 106

QY 113 QVEVLIDKKIEYAKSKALAELOGLQNNFEDVYVNALNSWKKTPLSLRSKRQDRIRELF 172
DB 107 HVEEIIINQKISTYARNKALTDLKGLDALAVYHDSLESVWG---NRNNTARSVVKSYI 163

QY 173 QAESHFRNMPSPFAVSKFEVLPLPTVYQAANTHLLLDKDAQVGEWGYSSDEVAEFYHR 232
DB 164 ALELMFVQKLPSFASGEEVPLPIYQAANLHLLLDASIFGKWLSEISSTFYNR 223

QY 233 QKLKLTQOYTDHCVMYVNGLVGLRGSTYDAWKFNFRREMTLTVLVDLVLFPFYDIRLY 292
DB 224 QVERAGDYSCHVKWYSTGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPFYDTQMY 283

QY 293 SKGVKTELTRDITFD-----PIFSLNT-LQEYGTPTLSIENS-IRKPHLFDYLOGIE 342
DB 284 PIKTTAQLTREVVYTDAGTGVHPHPSFTSTTWNNAAPSFALEAAVVRNPHLLDFLEQVT 343

QY 343 FHTRLQPGYFGKDSFNWYSGNVVETRPISGSKTITSPFYGDKSTEPVQKLSFDGQKYR 402
DB 344 IYSLLS-RWSNTQYNNMGGHKLFR-TIGGTLNISTQGSTNTSINPV-TLPFTSRDVR 400

QY 403 TIANTDVAAPNGKVLGVTKVDFSQYDDQKNETSTQYDSCRNGH-----VSAQDSIDQ 458
DB 401 TESLAGLNFLTPQVN-GVPRVDF-----HWKVTHTPIASDNFYPGYAGICTQLQDSNE 455

QY 459 LPPETTDPLEKAYSHQLNYAECLFMQDRRGITPFTTWTTHRSVDFNTIDAETITQLPV 518
DB 456 LPPEATGQPNVESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTEPNSITQPLV 513

QY 519 KAYALSSGASIIEGPQTCGNLLFLKESNSTAKFKVTLNSAALLQRYVRIRVASTNL 578
DB 514 KAPNLSGAAVVRGPGFTGGDIL-RTNTGTGDIRVNN-PPFAQRYVRIRVASTTDL 571

QY 579 RLFPVQ-----NSNNDPLVIYINKTNKDDDLTYOTEDLATNNSMGSGDKNELIIGAE 632
DB 572 QPHTSINGKAIQGN-----FSATNKGEDLDYKTFVTGFTTFPFLDQVSTFTTIGAW 625

```
Db 456 LPPEQTGPVYSHRLSHIGLSASHVKALV--YSWTHRSADRTNTIEPNSITQIPLV 513
QY 519 KAYALSSGASIIIEGPGFTGGNLLFLKESNSAKFKVTLNSAALLQVRVRIRYASTTNL 578
Db 514 KAFNLSSGAAVVRGPGFTGGDIL-RRNTGTGTGDIRVNIN-PPFAQRYVRIRYASTTDDI 571
QY 579 RLFFVQ-----NSNNDFLVIYINKTKMKNDDLTQYTFDLATNNSGFGSGDKNELIIGAE 632
Db 572 QFHTSINGKAINQGN-----FSATMNRGDDLYKTFRTVGTFTTFFPSFSDVQSTFTIGAW 625
QY 633 SFVSNKIIYIDKIEFIPVOL 652
Db 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 25
O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryV101;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 32.1%; Score 1094.5; DB 2; Length 719;
Best Local Similarity 36.5%; Pred. No. 5e-63;
Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

QY 1 MNPNNRSEHTI-----KVTNSELQNNHNOYPLADNPSTLELNKYEFLEMTEDSS 53
Db 1 MKLKNQDKHQSFSSNAKVKDISTDS-----LKNETDIELQNHEDCLKMSEYEN 50
QY 54 TE-VLDNSTVKAVGTSISVGGQILGVGVFPAGALTSEYQSFNTIWPSPDADPWKAFA 112
Db 51 VEPFVSASTIQ---TGIGIAGKILGTGLVPAGQVASLYSIFILGELWPKGNQWEIME 106
QY 113 QVEVLIDKIEEYAKSAEALQGLQNFEDVYNALNSWKTKPLSLRSKRSDRIELFSL 172
Db 107 HVEEIIINQKISTYARNKALTDLKLGDALAVHDSLESVVG---NENNTARSVVKQSYI 163
QY 173 QAESHPNMPSPAVSKFVFLFTVQAANTHLLLLKDAQVFGGEWGSVSDVAEYFHR 232
Db 164 ALELMFVQKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNR 223
QY 233 QLKLTQOYTDHCYNNVNGVLGRGSTDYDAWVKFNRFRREMTITVLDDLVLPPFYDIRLY 292
Db 224 QVERAGDYSDHCYKWKYSTGLNNLRGNTAESWRYNGFRRDMTLWLDLVALPFSYDTQMY 283
QY 293 SKGVKTELTRDFTD-----PIFSLNT-LQEYGTFLSIENS-IRKPHLFDYLGQIE 342
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Db 284 PIKTTAQLTREVVYDAIGTVHPSPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVT 343
QY 343 FHTLQPGYFGKDFPNYWSGNYVETRPSIGSSKTIITSPFYGDKSTERPQKLSFDGQKYR 402
Db 344 IYSLLS-RWSNTQTMNMWGGHKLFR-TIGTFLNISTQGSTNTSINPV-TLPFTSRDYR 400
QY 403 TIANTDVAAMPNGKYLGVTKVDFSQYDDQDNQSTSTQYDSKRNGH----VSAQDSIDQ 458
Db 401 TESLAGLNLFTQPN-GVPRVDF----HWKFVTHPTASDNFYPGYAGICTQLQDSENE 455
QY 459 LPPETTDEPLEKAYSHQNLNAYACFLMQDRRTGTFPFTWTHRSVDFNTIDAEKTLQLPV 518
Db 456 LPPEATGPVNESYSHRLSHIGLSASHVKALV--YSWTHRSADRTNTIEPNSITQIPLV 513
QY 519 KAYALSSGASIIIEGPGFTGGNLLFLKESNSIAKFKVTLNSAALLQVRVRIRYASTTNL 578
Db 514 KAFNLSSGAAVVRGPGFTGGDIL-RRNTGTGTGDIRVNI-KPPFAQRYVRIRYASTTDL 571
QY 579 RLFFVQ-----NSNNDFLVIYINKTKMKNDDLTQYTFDLATNNSGFGSGDKNELIIGAE 632
Db 572 QFHTSINGKAINQGN-----FSATMNRGDDLYKTFRTVGTFTTFFPSFSDVQSTFTIGAW 625
QY 633 SFVSNKIIYIDKIEFIPVOL 652
Db 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 26
C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbA (insecticidal delta-endotoxin
GN CryIb(a)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
OS Name=cryIbA; Synonyms=cryA4, cryIB(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RL Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X06711; CAA29898.1; -.
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DR EMBL; X95704; CAA65003.1; -.
DR PIR; S00873; S00873.
DR HSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y->H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D98575 CRC64;

Query Match      31.5%; Score 1072.5; DB 1; Length 1228;
Best Local Similarity 36.6%; Pred. No. 2.9e-61;
Matches 246; Conservative 120; Mismatches 247; Indels 59; Gaps 19;

QY 1 MNPNNRSEHDTIKVTPNSELQTNHNYPLADNPNTLLEELNYKEFLRMTDSSTEVLDNS 60
DB 1 MTSNRKNEEIIINAVNSHAQMD-----LLPDARIEDSLCIAEGNN--IDPF 45

QY 61 TVKDAGTGVSVVQIILGVGVFPAGALTSFYQSFLNTIWPSDADPKWAPMAQVEVLIDK 120
DB 46 VSASTVQTGINIAGRILGVLPFAGQLASFYSLVGLMWRGRDQWEIFLEHVEQLNQ 105

QY 121 KIBEYAKSKALAELOQNNFEDYVNALNSWKKTPLSLRSKRQDRIRE-LFSQ---AES 176
DB 106 QITENARNTALARLOGLGDSFRAYQOSLEDWLE-----NRDARTSRVLYTYQIALEL 158

QY 177 HFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVGEWGYSESDVAEYFHRQLK 236
DB 159 DFLNAMPFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVER 218

QY 237 TQOYTDHCYVNVYVGLNGLRGTYDAWVKNRFRREMTLVLDLVLFPYDRLVSKGV 296
DB 219 TRDYSYCVWEYNTGLNSLRGTNAASWVRYNQRRDLTLGLVDLVALFPYSYDTRTPINT 278

QY 297 KTELTRDIFDPTI-----FSLNTLQEGYPTLSIE-NSIRKPHLFDYLOGIEFHTRLQ 348
DB 279 SAQLTREYVTDALGATGVNMAWNNVNNAPSFAIEAAAIRSPHLLDFLEQLTIFS-AS 337

QY 349 PGYFGKDSFNYSNGVYETRPSIGSSKTTISPPYG--DKSTEPVQKLSFPGQKYRTIAN 406
DB 338 SRWSNTRHMTYWRGRTIQSRPIGGGLNTST--HGATNTSINPV-TLRFASRDVYRTESY 393

QY 407 TDVAAPNGKVKYL---GVTKVDFSQYDDQK-NETSTQTVDSKRNNGHVSQAQSIDQLPP 461
DB 394 AGVLLM---GIYLEPIHGVPTVRFTNPQNISDRGTANYSQPYESFGLQKDSLETLP 450

QY 462 ETTDEPLEKAYSHQLNVAECFLMQDRGTIPFTTWTTHRSVDFNTIDA EKITOLPVVKAY 521
DB 451 ETTERPNEYESYSHRLSHIGILOS--RVNVVYVSWTHRSADRNTTIGPNRITQIPWKAS 508

QY 522 ALSGASIIIEGPGFTGNNLLFLKESNSIAKFKVTUNSAALLQRYVRIRYASTTNLRLF 581
DB 509 ELPGQTTVVVRGPGFTGGDIL-RRNTNGGFGPIRVTVN-GPLTQRYRIGFYASTVDPDF 566

QY 582 VQNSN---NDELVIYINKTNKDDLLTYQTFDLATNTSNMGFGSGDKNELIIGAESFVNE 638
DB 567 VSRGGTTVNNFRFL---RTWNSGDELKYGNFVRAFTTPTFTTQIQDIIRTSIQGLSGNG 623

QY 639 KIYDKIEPIPV 650
DB 624 EVYDKIEPIPV 635

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RESULT 27

Q93NMS

ID Q93NMS PRELIMINARY; PRT; 1228 AA.

AC Q93NMS;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CylBa.
GN Names: cylBa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match      31.5%; Score 1071.5; DB 2; Length 1228;
Best Local Similarity 36.6%; Pred. No. 3.4e-61;
Matches 246; Conservative 119; Mismatches 248; Indels 59; Gaps 19;

QY 1 MNPNNRSEHDTIKVTPNSELQTNHNYPLADNPNTLLEELNYKEFLRMTDSSTEVLDNS 60
DB 1 MTSNRKNEEIIINAVNSHAQMD-----LLPDARIEDSLCIAEGNN--IDPF 45

QY 61 TVKDAGTGVSVVQIILGVGVFPAGALTSFYQSFLNTIWPSDADPKWAPMAQVEVLIDK 120
DB 46 VSASTVQTGINIAGRILGVLPFAGQLASFYSLVGLMWRGRDQWEIFLEHVEQLNQ 105

QY 121 KIBEYAKSKALAELOQNNFEDYVNALNSWKKTPLSLRSKRQDRIRE-LFSQ---AES 176
DB 106 QITENARNTALARLOGLGDSFRAYQOSLEDWLE-----NRDARTSRVLYTYQIALEL 158

QY 177 HFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVGEWGYSESDVAEYFHRQLK 236
DB 159 DFLNAMPFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVER 218

QY 237 TQOYTDHCYVNVYVGLNGLRGTYDAWVKNRFRREMTLVLDLVLFPYDRLVSKGV 296
DB 219 TRDYSYCVWEYNTGLNSLRGTNAASWVRYNQRRDLTLGLVDLVALFPYSYDTRTPINT 278

QY 297 KTELTRDIFDPTI-----FSLNTLQEGYPTLSIE-NSIRKPHLFDYLOGIEFHTRLQ 348
DB 279 SAQLTREYVTDALGATGVNMAWNNVNNAPSFAIEAAAIRSPHLLDFLEQLTIFS-AS 337

QY 349 PGYFGKDSFNYSNGVYETRPSIGSSKTTISPPYG--DKSTEPVQKLSFPGQKYRTIAN 406
DB 338 SRWSNTRHMTYWRGRTIQSRPIGGGLNTST--HGATNTSINPV-TLRFASRDVYRTESY 393

QY 407 TDVAAPNGKVKYL---GVTKVDFSQYDDQK-NETSTQTVDSKRNNGHVSQAQSIDQLPP 461
DB 394 AGVLLM---GIYLEPIHGVPTVRFTNPQNISDRGTANYSQPYESFGLQKDSLETLP 450

QY 462 ETTDEPLEKAYSHQLNVAECFLMQDRGTIPFTTWTTHRSVDFNTIDA EKITOLPVVKAY 521
DB 451 ETTERPNEYESYSHRLSHIGILOS--RVNVVYVSWTHRSADRNTTIGPNRITQIPWKAS 508

QY 522 ALSGASIIIEGPGFTGNNLLFLKESNSIAKFKVTUNSAALLQRYVRIRYASTTNLRLF 581
DB 509 ELPGQTTVVVRGPGFTGGDIL-RRNTNGGFGPIRVTVN-GPLTQRYRIGFYASTVDPDF 566

QY 582 VQNSN---NDELVIYINKTNKDDLLTYQTFDLATNTSNMGFGSGDKNELIIGAESFVNE 638
DB 567 VSRGGTTVNNFRFL---RTWNSGDELKYGNFVRAFTTPTFTTQIQDIIRTSIQGLSGNG 623

QY 639 KIYDKIEPIPV 650

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Db          624 EVYIDKIEIIPV 635
:::|||||
RESULT 28
Q93T75      PRELIMINARY; PRT; 1228 AA.
ID Q93T75
AC Q93T75;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.P., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF633025; AAKS1084.1; -.
DR HSSP; P07130; 1DEC.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0005952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; Endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF05555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DF59C95C3 CRC64;

Query Match 31.4%; Score 1070.5; DB 2; Length 1228;
Best Local Similarity 36.2%; Pred. No. 3.9e-61;
Matches 242; Conservative 123; Mismatches 252; Indels 51; Gaps 17;

QY 1 MNPNNRSEHDTTKVTPNSELQTNHQNQYPLADNPNTLBELNLYKEFLRMTESSSTEVLNS 60
DB 1 MTSNRKNEEIIIVNSNHSQAQMD-----LLPDARIEDSLCIAEGNN---IDPF 45
QY 61 TVKDAVGTSVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVLEVDK 120
DB 46 VSASTVQTGINAGILGVLPFAGQLASFYSFLVGLMPPRGDQWEFLFHEVQLNQ 105
QY 121 KTEEVAKSKALAELOGLQNPFEDYVNALNSWKKTPLSLRSKRSQDRIRFLFSQAESHFN 180
DB 106 QITENARNTALARLQGLGDSFRAYQOSLEDWLE--NRDDARTSRVLHTQYIALELDFLN 162
QY 181 SMPSAVSKFEVLPLFTYAQAANTHLLIKDAQVGEEMGYSSDVAEPYHRLKLTQOY 240
DB 163 AMPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQBIQRYERYQVTRDY 222
QY 241 TDHCYNNVNGLGRSGTYDAWKFNRPRRMTLTLDLIVLFPFYDIRLYSKGKTCL 300
DB 223 SDYCVENWTGLNSLRGTNAASWVYNQPRDLTLGLDLVALFPSTYTRITYNTSACL 282
QY 301 TRDIFTDPI-----FSLNTLOEQYPTPLSTE-NSIRKPHLFDYLOQIEFHRLQPGYF 352
DB 283 TREVYTDAGATGVNNAASWNNYNNAPSAIEAAAIKSPHLLDLEQLTIFS-ASSRWS 341
QY 353 GKDSFNYSNGVNEVTPSPISGSKTITSPPYG--DKSTEPVQLKSPDGQVYRTIANTDVA 410
DB 342 NTRHMTYWRGTHIQSRPIGGGLNTST---HGATNTSINPV-TLRFASRDVYRTESYAGVL 397
QY 411 AWPNGKAVYL----GVTKVDFSDYDQK-NETSTQYDSCRNNGHVSAQDSIDQLPPETTD 465
DB 398 LW---GIVLEPHGVPTVRFTNPNQINSDRGNTANYSPQESPGQLKDSLELPEPTE 454
QY 466 EPLEKAYSHQLNASCFLMQDRRGITPFTTWRHSVDFNTIDASKITQLPVPVKAYALSS 525
:::|||||
```

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Shu C., Zhang J.;

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DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE CryiBII.
GN Name=cryiBII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Isakova I.A., Isakov Y.B., Rymar' S.E., Yarovoi S.V.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV139457; AAM93496.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1231 AA; 139764 MW; C9F2848A9297TEA00 CRC64;

Query Match 30.7%; Score 1053; DB 2; Length 1231;
Best Local Similarity 36.1%; Pred. No. 5.5e-60;
Matches 243; Conservative 114; Mismatches 261; Indels 56; Gaps 17;

QY 1 MNPNNRSEHDTIKVTPNSELQTNHQYPLADNPSTLELNKKEFLRMTEDS----STEV 56
DB 1 MTSNRKNENEII-----NALSIPTVSNPST---QMNLSPDARI-EDSLCVAEYNN 46

QY 57 LNSTVKDVGAGTGISVVGQILGVGVPPFAGALTSPYQSFINTWPSDDADPWKAFMAQVEV 116
DB 47 IDPFVSASTVQTGINAGRIILGVGVPPFAGALSFYSLVGLWPSGRDPWFIFLEHVQ 106

QY 117 LIDKKEEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRKSQDRIRLEFSQAES 176
DB 107 LIRQOVQTRNTATRLGLEGRGYSYQOALETLDL---NRNDARSIIILERYVALEL 163

QY 177 HFRNSMPSFAVSKFEVLFTPYAQANLHLLKDAQVGEWGYSSSEDVAEFYHROLKL 236
DB 164 DITTAIPLFRIRNEEVPLLMVYQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRY 223

QY 237 TQOYTHCVNWNVLNGLRGSTYDAWKFNFRREMTLTVLDLVLFFYDIRLYSKGV 296
DB 224 TBEYSNHCQVWYNTGLNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSTYDTRTPINT 283

QY 297 KTELTRDIFTDPI-----FSLNTLOEYGPFTLSIENSI-RKPHLPDYLOGIEFHTR 346
DB 284 SAQLTREIYTDPIGRTNAPSGFASSTWNNNAPSFSAIEAALFRPPLLDPFEQLTIYS- 342

QY 347 LQPGYFGKDSFNWNGYVETRPISGSKTITSPFYGDKSTBFPVKLSFDGQKVRTIAN 406
DB 343 ASSRWSSTQHMVWVGHRLNFRPIGTLNTSTQGLTNNTSINPV-TLQFTSRDVRTESN 401

QY 407 TDVAAMPNGKVLGVTKVDFPSQVD-----DQKV--ETSTQTVDSKRNHGVSAQSIDOL 459
DB 402 A-----GTNLFTFTPVNGVPWDRFNFINPQNIYERGATTYSQPYQGVGIQLDFSETEL 454

QY 460 PPETDEPLEKAYSHOLNAECLFMQDRRGITPFFTWTHRSVDFNTIDAEKITQLPVVK 519
DB 455 PPETTERPNVESYSHLSHIGLIIGNTLRA--PVYSWTHRSADRTNITGNRIQTIPAKY 512

QY 520 AYALSSGASIIIEGPGFTGGNLLFLKBSNSIAK---FKVTLNSAALLQRYVRIRYASVT 576
DB 513 GRFLFNG-SVIGSGPGFTGGDVRLNRNGNIQNRGIEVPIQFTSTSTRYVRVRYASVT 571

QY 577 NLRLFVQNSNDPLVIYINKTKMKDDLLTYQTFDLATTNSMFGSGDKNELIIGAESFVS 636
DB 572 STELVNVLGNSSIFTNTLPATAASLNL--QSGDFGVYVEINNAFTSATGN-IVGARNFSA 628
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QY 637 NEKIYIDKIEFIPV 650
DB 629 NAEVIIDRFEPFIPV 642

RESULT 32
CLIC_BACTU
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=c18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF056933; AAC62933.1; -
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 30.7%; Score 1046.5; DB 1; Length 719;
Best Local Similarity 35.4%; Pred. No. 6.9e-60;
Matches 243; Conservative 130; Mismatches 238; Indels 75; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNSELQTNHQYPLADNPSTLELNKKEFLRMTESS 53
DB 1 MKLKNPDKHQTLSSNAKVDTKATDS-----LKNETDIELKMNEDYLRMSEHS 50

QY 54 TEVLDSNTVKDVGAGTGISVVGQILGVGVPPFAGALTSPYQSFINTWPSDDADPWKAFMAQ 113
DB 51 ---IDPFVSASTVQTGINAGRIILGVGVPPFAGALSFYSLVGLWPKGKSQWEIFMEH 107

QY 114 VEVLIDKKEEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRKSQDRIRLEFSQ 173
DB 108 VEATINRKISTYARNKALTDLKGLGDALAVHESLESVWG---NRNTRARSVVRKNQYIA 164

QY 174 AESHPFNMSPSFAVSKFEVLFTPYAQANLHLLKDAQVGEWGYSSSEDVAEFYHRO 233
DB 165 LELMFVKQLPSPFVSGSEVFPLLPIYQAANLHLLLRDASIFPKNGGLSASEISTFYNRQ 224
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Db 121 ELIDQRISEQVWALDALTGIHDYNYEYLALEEMLERENGARANLAFQ-----PENLH 176
Qy 176 SHFNSPSP-----AVSKFEVLFLPTTAAQANLHLLKDAQVFGEBWGSSEDAEFPYH 231
Db 177 QLFVSQMPSPGSGPGRDAVALLTVYAAQANLHLLKDAEYGARWGLNQGINLYFN 236
Qy 232 RQLKLTQOYTDHCVNMYNGLNGRSTYDAWKFNFRREMTLTVLDLVLFPFYDIRL 291
Db 237 AQDRQIYTNHCVATYRGLNLRGTNTESWYNYHQFRREMTLMANDLVALFPYNLQ 296
Qy 292 YSKGVKTELTRDIFTDFISLNTLQEY-----PTFLSIENS-IRKPHLFDYLOG 340
Db 297 YPGANPQLTREIYTDVW-FNPPANQGLCRWRNNPYMTFSELENTFIRPHLFDRLNS 355
Qy 341 IEFHTRLPQCYFGKDSFNYSNGYVETRPISGSKTITSFPYGDKSTEPVKLSFQGV 400
Db 356 LTINSHRFP-----ISGNFMYWAGH-----TLRRSYMNSA---VOEDSYGATTS 398
Qy 401 YRTIANTDVAAPNGKYLGVTKVDFSQ-----YDQK-----NETSTQTYDSKRN 446
Db 399 TRVTINTGV-----NGTNRIESTAVDFRSGLLGVYGVHRASFVPGGLFNGTI-----SPAN 449
Qy 447 NGHVSQADSIDQLP-PETTDEPLEKAYSHQUNYAECL--MQDRRGTI-----PFFTWT 497
Db 450 AGCRNLHTRDELPLEENNGSP-----SHRLSHV-TFLSLTDOAGSIRNSGAVPLYWA 503
Qy 498 HRSVDPFNTIDAEKITOLPVVKAVALSSGASIIEGPGFTGCGNLLFLKESNSIAKPKVTL 557
Db 504 RQIDLNLNTITANRIITOLPLVKAASEATAAGTVVRGPGFTGCGDIL-RTSAGTIGTIRVNV 562
Qy 558 NSAALLQRYVRIRYASTTNLRLFVQNSNNDLVIYINKTMKDDDLTYOTFDLATTNSN 617
Db 563 NS-PLQRYVRIRYASTTNDFNFVIRGGTVVNFPTPTMNSGQSESYVYTRFESTS 621
Qy 618 MFGSGDKNELIIGAESFVSN-----EKIYIDKIEPIV 650
Db 622 FNFELQIDTLRLTVQSFSSQGVVDRIEIIPV 654

RESULT 36
Q6PYW8
ID CIBE_BACTU PRELIMINARY; PRT; 849 AA.
AC O6PYW8;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE CrylB type crystal protein (fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY50734; AAS93797.1;
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON TER 849
SQ SEQUENCE 849 AA; 95886 MW; FCB98495787CF763 CRC64;

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Query Match 29.7%; Score 1013; DB 2; Length 849;
 Best Local Similarity 34.9%; Pred. No. 1.4e-57;
 Matches 243; Conservative 123; Mismatches 226; Indels 104; Gaps 23;

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Qy 1 MNPNNSEHDTIKVTPNSELOTHNQYPLADNPSTLE---ELNYKEFLRWTESSTEVL 57
Db 1 MTSNRKNENIIL-----NALSIPAVNSHAQNNLSTDAKIEDSLCIAEGNN---I 47
Qy 58 DNSTVDKADVTGTSVVGQILGVGVFPAGALTISFYQSLNTIWPSPDADPWKAFMAQVEVL 117
Db 48 DPFVSASTVQTGINIAGRILVLGVFPAGQIASFYSLVGLMWRGRDPEIFLEHVEQL 107
Qy 118 IDKKIEEYAKSALAELOGLNPNFEDYVNAINLWKTPLSLRSKRSQDRIRE-LFSQ--- 173
Db 108 IRQQVNTTRDTALARLOGLNSFRAYQOSLEDWLE-----NRDDARTSRVLTQYIA 160
Qy 174 AESHFNSMSPSPAVSKFEVLFLPTTAAQANLHLLKDAQVFGEBWGSSEDAEFPYH 233
Db 161 LEUDFLNAPLFAIRNQEVPLLMVYAAQANLHLLKDAEYGARWGLNQGINLYFN 220
Qy 234 LKLTQOYTDHCVNMYNGLNGRSTYDAWKFNFRREMTLTVLDLVLFPFYDIRLS 293
Db 221 VEKTRSYDYCARWYNTGLNLRGTNAESWLRYNQFRRLDTLGLVLDLVALFPSTYDTRVP 280
Qy 294 KGVKTELTRDIFTDPI-----PSLNTLQYEGTFLSIENS-IRKPHLFDYLOGIEP 343
Db 281 MNTSAQLTREIYTDPIGRTNAPSGFASTNWFNNAPSFSAIEAAVIRPPHLLDFPEQLTI 340
Qy 344 HTRLPQCYFGKDSFNYSNGYVETRPISGSKTITSFPYGDKST--EPVKLSFQGV 401
Db 341 FSVLS-RWNTQYMYNVWGHRLSRTIRGSLSTST---HGNWTISNPV-TLQFTSRDVP 395
Qy 402 RT-----IANTDVA-----WPN-----GKVY-LGVTKVDFSDQYDQKNETST 438
Db 396 RTESFAGINILLTTPVNGVPWAFNRNPLNSRGLLTYIGTVG-----GT 443
Qy 439 QYVDSKRNNGHVSQAQSIDQLPPTTDEPLEKAYSHQUNYAECLMQDRRGTIPTFTWTH 498
Db 444 QLFDS-----TELPPETTERPNYESYSHRLSNIR--LISGNTLRAPVYSWTH 489
Qy 499 RSVDFPNTIDAEKITOLPVVKAVALSSGASIIEGPGFTGCGNLLFLKESNSIAKPKVTLN 558
Db 490 RSDRTNTTSSDSITQIPLVKSFNLSGTSVSGPGFTGCGDII-RTNNGSVLSMGLNPN 548
Qy 559 SAALLQRYVRIRYASTTNLRLFVQNSNNDLVIYINKTMKDDDLTYOTFDLATTNSN 618
Db 549 NTS-LQRYVRIRYAAASQTMVLRVTVGGSTTPDQGFPTMSANESLTSQSFRFAEPVGI 607
Qy 619 GFGSGDKNELIIGAESFVSN-----EKIYIDKIEPIV 650
Db 608 SASGSQT-----AGTISNNAGRQTFHDKIEPIPI 638

RESULT 37
CIBE_BACTU
ID CIBE_BACTU STANDARD; PRT; 1227 AA.
AC O8505;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein crylBe (Insecticidal delta-endotoxin  

  CrylB(e)) (Crystalline entomocidal protoxin) (139 kDa crystal protein).  

OS Bacillus thuringiensis.  

OG Plasmid pMVC2383.  

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  

OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.  

RC STRAIN=NRRL B-18872 / PS158C2;  

RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;  

RL "Bacillus thuringiensis genes encoding lepidopteran-active toxins.";  

CC Patent number US5723758, 03-MAR-1998.  

CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut  

  epithelial cells of many lepidopteran larvae.  

CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during

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sporulation and is accumulated both as an inclusion and as part of the spore coat.

CC MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.

CC

CC -!- SIMILARITY: Belongs to the delta endotoxin family.

CC

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CC

CC -----

CC EMBL: AF077326; AAC32850.1; --

CC HSSP: P07130; IDLC.

CC InterPro: IPR001178; Endotoxin.

CC InterPro: IPR005638; Endotoxin_C.

CC InterPro: IPR005639; Endotoxin_N.

CC InterPro: IPR008979; Gal bind like.

CC Pfam: PF03944; Endotoxin_C; 1.

CC Pfam: PF00555; Endotoxin_M; 1.

CC Pfam: PF03945; Endotoxin_N; 1.

CC Plasmid; Sporulation; Toxin.

CC KW

CC SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;

CC

Query Match 29.7%; Score 1013; DB 1; Length 1227;
Best Local Similarity 34.9%; Pred. No. 2.3e-57;
Matches 243; Conservative 123; Mismatches 226; Indels 104; Gaps 23;

QY 1 MNPNNRSEHDTIKVTNSELOTHNNOYPLADPNSTLE---ELNYKEFLRMTEDSDSTEVL 57
DB 1 MTSNRKNEIIL-----NALSIPAVNSHSAQMNLSTDAIEDSLCIAEGNN---I 47

QY 58 DNSTVKDAGTGISVVGQILGVGVPFAGALTSFYQSFLNTTWPSDADPWKAFMAQVEVL 117
DB 48 DPFVSASTVQTGINAGRIILGVLPVAGQIASFYSFLVGLWPRGRDPWEIFLEHVEQL 107

QY 118 IDKTEEVAKSKALAELOGLQNNFEVDYNALNSWKTPLSLRSKSQDRIRE-LFSQ--- 173
DB 108 IQQVTEVTRDTALARKLGLGNSFRAYQQSLSDWLE-----NRDDATRSVLTYQYIA 160

QY 174 AESHFRNSMPSFAVSKFEVLFLEPTAQAAANTHLLLLKDAQVFGEEGWYSSSDVAFYHRQ 233
DB 161 LELDFLNAMPEFAIRNOEVPFLMVYQAANLHLLLRDASLFGSEFGLTSQEIQRVYERQ 220

QY 234 LKLTQQYTDHCYNNVNVGLNGRSTYDAWVKNFRREMTLTVDLVLFPFYDIRLYS 293
DB 221 VEKTRYSYDCARWYNTGLNNLRGTNAESWLRYNQFRRLDTLGLVLDLVALPFSYDTRVYP 280

QY 294 KGVKTELTRDIETDPI-----FSLNTLQYGTFTLSIENS-IRKPHLPDYLGQIEF 343
DB 281 MNTSAQLTRIEITYDPIGRNAPSGASTNWFNNAFSAISAAVIRPPLLDFPEQITI 340

QY 344 HTRLPQGVFGKDSFNWNGSNVYETRPSGSKTITSPPFGDKST--EPVOKLSFDQKVY 401
DB 341 FSVLS-RWSNTQYMNKVVWGHRELSRTIGSLSTST--HGNTNTSINPV-TLQFTSRDVP 395

QY 402 RT-----IANTDVA-----WPN-----GKVV-LGVTKVDFSQYDDQKNETST 438
DB 396 RTESFAGINILUTTPVNGVFWARFNRNPLNSLRGSLTYITGTG-----GT 443

QY 439 QTYDSKRNGHVSQAQSDIDQLPPETDDEPLEKAYSHQNLNARCFMLQMDRRGTIPFFTWTH 498
DB 444 QLFDSE-----TELPETTERPNYESYSHRLSNIR--LISGNTLRAPVYSWTH 489

QY 499 RSVDFNFNIDAKITQLPVVKAYALSSGASIEGPGFTGGLNLLFKESNSIAKPKVTIN 558
DB 490 RSADRTNTISSDITQIFLVKFSNLNSGTSVVSGFGFTGGDII-RTNVNGSVLSMGLNFN 548

QY 559 SAALLQRYVRIRYASTTNLRFLVQNSNNDPLVVIYNKMKDDLTQYTFDPLATNSNM 618
DB 549 NTS-LQRYVRVRYAASQTMVLRVTVGGSTTFDQGFPPMTMSANESLTSQSFRAEPFVGI 607

QY 619 GFSGDKNELIIGAESFVN-----EKIYIDKIEFIPV 650
DB 608 SASGSQT-----AGISISNAGROTFFHFKIEFIDI 638

RESULT 38
Q9S603 PRELIMINARY; PRT; 645 AA.
ID Q9S603;
AC Q9S603;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serovar japonensis type;
RX MEDLINE=99025985; PubMed=9806979;
RA Wasano N., Ohba M.;
RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific
RT Bacillus thuringiensis strains that produce spherical parasporal
RT inclusions.";
RL Curr. Microbiol. 37:408-411(1998).
DR EMBL; AF042733; AAB97923.1; --.
DR HSSP; P07130; IDLC.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; Endotoxin_C.
DR InterPro; IPR005639; Endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON_TER 1 645
FT NON_TER 1 645
SQ SEQUENCE 645 AA; 72967 MW; 143E51312B890CE3 CRC64;

Query Match 29.3%; Score 999.5; DB 2; Length 645;
Best Local Similarity 34.8%; Pred. No. 7e-57;
Matches 230; Conservative 114; Mismatches 248; Indels 69; Gaps 16;

QY 26 QYPLADNPSTLEELNYKEFLRMTEDSDSTEVLDSNV----KDAVGTGISVVGQILGVVG 81
DB 11 KYPLTDDPNAGLQNNMYKEYLQTYGGDYTDPLINPNLSVSGKDVQVGINIVGRLLSPFG 70

QY 82 VPEAGALTSFYQSFLNTTWPSDADP-WKAFMAQVEVLIDKIEEVAKSKALAELOGLQNN 140
DB 71 PFFSQWTVVTVYLLNSLWPDDENSVMDAFMERVEELIDQKISEAVKRALDLDLTGLQYN 130

QY 141 FEDVYNALNSWKTPLSLRSKRSQDRIRELFSQAESHFNSMPSF-----AVSKFEVFLP 196
DB 131 YNLVYEALEDWLNRPNGARASIVSQR----FNILDSLTFQWPFSGSGFQSNYATILLP 186

QY 197 TYAAQANTHLLLLKDAQVFGEEGWYSSSDVAFYHRQLKLTQQYTDHCYNNVNVGLNGLR 256
DB 187 VYAAQANLHLLLLKDAQVFGEEGWYSSSDVAFYHRQLKLTQQYTDHCYNNVNVGLNGLR 246

QY 257 GSTYDAWVKNFRREMTLTVDLVLFPFYDIRLYSKGVKTELTRDITFTDPIFSLNTLQ 316
DB 247 GTTAESEFKYQYRREMTLTAMDILVALFPYYNLQYPDGTNPQLTRREYVTDPI-AFDFLE 305

QY 317 EYGT-----FLSIENS-IRKPHLPDYLGQIEFHTRLQPGVFGKDSF 357
DB 306 Q--PTTQLCRSWINPAFRNHLNFSVLNLSLRPHLFLERLSNLQILVNYQ-----TNG 357

QY 358 NYWNGNVYETRPSIGSSKTTITSPFGDKSTFVQKLSFDQGVKVRTTANTDVAAMPKGV 417
DB 358 SAWRGSRV--RYHYLHSSIIQEKSYGLLSDPVGANINQNNNDIYQIISQVSNFASPVGSS 415


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DR InterPro: IPR005638; endotoxin C.
DR InterPro: IPR005639; endotoxin N.
DR InterPro: IPR008979; Gal_bind_Like.
DR Pfam: PF03944; Endotoxin C; 1.
DR Pfam: PF00555; Endotoxin M; 1.
DR Pfam: PF03945; Endotoxin N; 1.
SQ SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;

Query Match 29.2%; Score 995; DB 2; Length 1150;
Best Local Similarity 33.8%; Pred. No. 3.le-56;
Matches 232; Conservative 124; Mismatches 258; Indels 72; Gaps 17;

QY 1 MNPNNRSHDITKVTNPSELQTNHNOYPLADNPSTLSEELNYKEFLRTMETSSTVLONS 60
DB 1 MRRNNPEYIIDAECYCGPDDVRYPLASDPNAAFQNMNYKEYLYQYDGYTGSLLNP 60

QY 61 TV---KDAVGTGISVVGQILGVVGVFPAGALTSFYQSLNTIWP-SDADPWKAFMAQVE 115
DB 61 NLSINPRVLTQGINIVGRILGFLGVPFAGQLVTFYTLNLQNLWTFNDNAVWEAFMAQIE 120

QY 116 VLIDKIEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRQDRIELFSQAE 175
DB 121 ELIDOKISAAQVVRNALDDLTGLHDYEEYLAALAEWLERPNGARA----NLVTQRFENLH 176

QY 176 SHFRNSMPSFAV----SKFEVLFLPTYAQAAANTHLLLLKDAQVFGEEGYSSEDAVEFYH 231
DB 177 TAFVTRMPSFGTGPQSGORDAVALLTVYQAANLHLLLLKDAIYGARWGLQCGQINLFPN 236

QY 232 RQLKLTQOYTDRHCNVNMYNGLNGRGSTYDAWVKFNFRREMTLTVLDLIVLFPFYDIRL 291
DB 237 AQQERTIVYTHCVETVYNGRLEDVRGTNTESWLVNHRFRREMTLAMDLVALFPFYVNRQ 296

QY 292 YSKGVKTELTRDITFDPIPSLNTLQEQYGP-----TFLSIENS-IRKPHL 334
DB 297 YPNGANPQLTREIYTDPIV-----YNPPANQGCIRWGNPNPYTFSELENAFIRPPHL 349

QY 335 PDYLGQIEFHTRLQPCYFGKDSFNWGSNGYVTRPSIGSKTITGPFYGDKSTEPVQKLS 394
DB 350 FERLNLITISNRHYTAPTNSFLDWSGHTLQSQHA--NNPTYTSGQITSTRLFTNT 407

QY 395 PDGQKYRTIANTDVAAMPNGKYLGVTKVPDSQYDDQKNETSQTYPYSKRNNGHVSAQD 454
DB 408 TNGARA-----IDSKARNFGNLYANLYGV-----SSLNIPPTGMSEITNAATCRQD 455

QY 455 SIDQLPPTTDE-PIEKAYSHQNLNVAECFLMQDRR-----GTIPFFTWTHRSVDFFNT 506
DB 456 L-----TTTEELPLENNNNFLLSHVTLFRFNTTQGGPLATLGFVPTVYVWTRREDVDFTNT 509

QY 507 IDAEKITQLPVVKAYALSSGASIIEGPGFTGNNLLFLKSSNSIAKFKVTLNSAALLQRY 566
DB 510 ITADRIQLPWKASEIGGTTVVKGPGFTGGDIL-RRTDGAVGTIRANVN-APLTQQY 567

QY 567 RVIRIYASTN--LRLFVQNSNDDFLVIYINKTMKDDLTQYTFDLATTSNMGFGSGDK 624
DB 568 RIRLRYASTTSFWNLFVNNSAAGFT--LPSTMAQNGSLTSEFNTLEVTHTIRFSQSD 624

QY 625 NELIIGAESFVNEKIYIDKIEPIV 650
DB 625 TTRLNLNIPFSISGQEVYVDKLEIVPI 650

RESULT 41
CQAA_BACTF STANDARD; PRT; 1163 AA.
AC Q9X597;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry26Aa (Insecticidal delta-endotoxin
DE CryXXVIA(a) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN Name=cry26Aa; Synonyms=cry26Aa1, cryXXVIA(a);
OS Bacillus thuringiensis (subsp. finitimus).
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OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_taxID=29337;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=VKPM B-1166;
RX MEDLINE=99330166; PubMed=10403372; DOI=10.1016/S0014-5793(99)00650-X;
RA Wojciechowska J.A., Lewitin E., Revina L.P., Zalunin I.A.,
RA Chestukhina G.G.;
RT "Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
RT thuringiensis ssp. finitimus.";
RL FEBS Lett. 453:46-48(1999).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF122897; AAD25075.1; -.
DR HSSP: P07130; 1DLG.
DR InterPro: IPR001178; Endotoxin_C.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR InterPro: IPR008979; Gal_bind_Like.
DR Pfam: PF03944; Endotoxin C; 1.
DR Pfam: PF00555; Endotoxin M; 1.
DR Pfam: PF03945; Endotoxin N; 1.
KW Direct protein sequencing; Sporulation; Toxin.
SQ SEQUENCE 1163 AA; 131284 MW; 72B5D5EB51341908 CRC64;

Query Match 28.6%; Score 975; DB 1; Length 1163;
Best Local Similarity 33.8%; Pred. No. 6.4e-55;
Matches 235; Conservative 130; Mismatches 247; Indels 84; Gaps 23;

QY 1 MNPNNRSHDITKVTNPSELQTNHNOYPLADNPSTL---BEL--NYKEFLRMTSDSSTE 55
DB 1 MNSEMHNVNPFSEISDNDNDVSIPOQRYFPANDPADSVFCADDFLQSYGEFNMDFGESEP 60

QY 56 VLDNSTVTKDVGTVGTISVVGQILGVVGVFPAGALTSFYQSLNTIWP-SDADPWKAFMAQV 114
DB 61 FIDAS---GAINAAIGVTGTVLGFLGVFPAGALTTFFYQKFLGFLFPNNNTKQWEEFMQV 117

QY 115 EVLIDKIEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRS---QDRIELF 171
DB 118 EALIDEKISDAVRNKAISELOGLVNNITLYTEALEW-----LENKENPAVRDVLQRW 171

QY 172 SQAESHRNSMPSFAVSKFEVLFLPTYAQAAANTHLLLLKDAQVFGEEGYSSEDAVEFYH 231
DB 172 RILDGFFEQQMPSPFAVGKFEVLLLVYVYQANLHLLSLRDVAYIYAEWGLTFTNDQHT 231

QY 232 RQLKLTQOYTDRHCNVNMYNGLNGRGSTYDAWVKFNFRREMTLTVLDLIVLFPFYDIRL 291
DB 232 RLLRHSABEYTDHCNVNMYNGLKQLENSDAKSWFQYNNRFRREMTLSVLVDIALFPAYDVKM 291

QY 292 YSKGVKTELTRDITFDPI-----FSLNTLQEQYGPFTLSIENS-IRKPHLFDYLO 339
DB 292 YPIPTNFQLTREVYTDVIGKIGRNDSDHWYSAN-----APSFNSLESTLIRTPHVVDYIK 346

QY 340 GIE--FHTRLQPGYFGKDSFNWGSNGYVTRPSIGSKTITSPFFYGDKSTEPVKLSFPG 397
DB 347 KLFYATVVDYIGYGRS--GKVVGHIIITSATNTETRN---YGTIVNHDSEVLNFEQ 401

QY 398 QKVYRTIANTDVAAMPNG-----KVVLGVTKVDFSQYDDQKNETSQTQYDSKR-- 445
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Db 402 KNIYKT-----GSLPQGVPPYQIGYVTPYFTRAVNFFTVSGSK--TSVEKYYSKDR 453
Qy 446 --NNGHVSAD--SIDOLPPETTDPELEKAYSHOLNVAECFLMDRR---GTIPFFTWTH 498
Db 454 YSEGLPEEOGVFTEQLPNPNSIAEPBHIAYSRHLCHVTTFISVNGNKYSKDLPLFSWTH 513
Qy 499 RSVDFNTIDAETITQLPVVKAYALSSGASIEGPGFTGGNLLPLKSSNSIAKFKVTLN 558
Db 514 SSVDFNVVYPTKITQLPATKY---NVSIVKEPGFIGDI--GKNGQILGKYKNVE 567
Qy 559 SAALLQRYVRIRVASTNLRFLVQNSNDDFLVIYINKTNKDDDLTYQTFDLATNSNM 618
Db 568 DVS--QKRYRFRVRYATEGELGKIDGRTVNLVYQYKTKRAGPDPLTYKAFDYLSPSTPV 625
Qy 619 GFSGDKNELIIGAESFVSNE---KIYIDKIEFIPVQ 651
Db 626 KFNASSTI-----ELFLQNKTSGTFYLAGIEIIPVK 657

RESULT 42
Q45745
ID Q45745 PRELIMINARY; PRT; 1144 AA.
AC Q45745
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin (Fragment).
GN Name: cryIX gene.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94085596; PubMed=8262221; DOI=10.1016/0014-5793(93)81613-5;
RA Shevelev A.B., Svarinskoy M.A., Karasin A.I., Kogan Y.N.,
RA Chestukhina G.G., Stepanov V.M.;
RT "Primary structure of the cryX**the novel Delta-endotoxin-related
RL gene from Bacillus thuringiensis ssp. galleriae.";
RN [2]
RP SEQUENCE FROM N.A.
RA Shevelev A.B., Kogan Y.N., Kuryatov M.V.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X75019; CAA52927.1; -.
DR PIR; S39536; S39536.
DR HSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; Endotoxin_C.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON_TER
SQ SEQUENCE 1144 AA; 129398 MW; 7D28594A19C4B065 CRC64;

Query Match 28.3%; Score 963.5; DB 2; Length 1144;
Best Local Similarity 33.3%; Pred. No. 3.6e-54;
Matches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;

Qy 41 NYKEFLMTE--DSSTEVLDSNVKDAVGTGISVVGQILGVGVVFPFAGALTSFVQSPLNTI 99
Db 19 SYKDYLMSEGDYIDSYINFGNVRTGLQTDIDIVAVVVGALGPGVGGILTGFLSTLFGFL 78
Qy 100 WPS--DADPWKAFMAQVEVLIDKIEEYAKSLAEQLQGNPNFEDVYNALNSKTKPLSL 158
Db 79 WPSNDQAWAEAFTEQMEELIEQISQVVRTALDLDLTGIGNYQNYLIAKWEERPNGV 138
Qy 159 RSKRSQDRIRLELFSQAESHFRNMPSPF---AVSKFEVLPLTPYQAANTHLLLLKDAQV 214

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Db 139 RA-----NLVLRFEILHALFVSMPSFGSGQSFQALLVVYQAANLHLLADAER 194
Qy 215 FGSEWGYSSDDVAEFYHRQLKL--TQYTDHCVMYVNVGLNGLRGSTYDVAWVKFNRFRRE 273
Db 195 YGARWGLRESQIGNLYFNEQLQTRDYTNHCVNAYNGLAGLGRGTSAESMLKYHQFRREA 254
Qy 274 TLAVLDLIVLPFVVDRLYSKYVKTELTRDIFTDP-----IFSLNTLOEYGP 320
Db 255 TLMAMDLIALFPYNTYRTRPIAVNPQLTREYVDPLGVPSSESLFPELRLCRLRWQETSAM 314
Qy 321 TFLSIENS--IRKPHLFYDLOGIEFHTLQPGYFGKDSFNWGSNGYVETREPSIGSSKTI 379
Db 315 TFSLENALIISSPHLEFDINNMIYTGSPSVHLTNQLEGMHGSVTSLLASGPTTVLR 374
Qy 380 PFYGDKSTEPVKLSFDGQKYYR--TIANTDVAAMPNGKYVLGVTKVDFSOYDDQKNETS 437
Db 375 RNYG-STTSIVNYFSDNRDQVYQINRSHSTGL--GFQNAPLF-GITRAQF-----YP 422
Qy 438 TOTYDSKRNGHVSQAQ--DSIDOLPPETTDPELEKAYSHOLNVAECFL-----MODR 487
Db 423 GGTYSVTQRMALTCQYNSIDELPSLDNPEISRSYSRHSHTSVLHRLVLTIDGINY 482
Qy 488 RGTIPPTWTHRSVDFNTIDAETITQLPVVKAYALSSGASIEGPGFTGGNLLFLKSS 547
Db 483 SGNLPTVWTHRDVLTNTITADRIITQLPLVKSFEIPAGTTVVRGPGFTGGDIL--RTGV 541
Qy 548 NSIAKPKVTLNSAALLQRYVRIRVASTNLRFLVQNSNDDFLVIYINKTNKDDDLTYQ 607
Db 542 GTEGTIRVR--TTAPLTQRYRIRFRASTTNLFTGIRVGRQVNYFDFRTMNRGDELYE 600
Qy 608 TFDLATNNSMGFGDKNELIIGAESFVSNEKIYIDKIEFIPV 650
Db 601 SFATREFTDFNRPQDELISVFANAFSAGQEVFDRIEIIPV 643

RESULT 43
C1CA_BACTE
ID C1CA_BACTE STANDARD; PRT; 1189 AA.
AC P05518; P10327; Q03742; Q45725;
DT 01-NOV-1988 (Rel. 09, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin
DE CryIC(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).
GN Name: cryIIa; Synonyms: cryIC, cryIC(a);
OS Bacillus thuringiensis (subsp. entomocidus), and
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436, 1433;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=60.5;
RX MEDLINE=88289380; PubMed=3399402;
RA Honee G., van der Salm T.P.M., Visser B.;
RT "Nucleotide sequence of crystal protein gene isolated from B.
RT thuringiensis subspecies entomocidus 60.5 coding for a toxin highly
RT active against Spodoptera species.";
RL Nucleic Acids Res. 16:6240-6240(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=NRRL B-18484 / PS811;
RA Payne J.M., Sick A.J.;
RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
RT genes encoding novel lepidopteran-active toxins.";
RL Patent number US5246852, 21-SEP-1993.
RN [3]
RP SEQUENCE OF 1-823 FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=7-29;
RX MEDLINE=89343627; PubMed=2548060;
RA Sanchis V., Lerechus D., Menou M., Chaufaux J., Guo S., Lecadet M.-M.;
RT "Nucleotide sequence and analysis of the N-terminal coding region of
RT the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis

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RT aizawai 7.29.";
RL Mol. Microbiol. 3:229-238(1989).
RN [4].
RP SEQUENCE OF 1-756 FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=7-29 / K26-21;
RA Strizhov N.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae including Spodoptera
CC species.
CC !- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC !- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC !- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X07518; CAA30396.1; -
CC EMBL; M73251; AAA22343.1; -
CC EMBL; X13620; CAA31951.1; -
CC EMBL; X96682; CAA65457.1; -
CC FIR; S00944; S00944.
CC FIR; S04181; S04181.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
CC CONFLICT 124 124 A -> E (in Ref. 1).
CC CONFLICT 294 294 A -> R (in Ref. 1).
CC CONFLICT 366 366 N -> I (in Ref. 3).
CC CONFLICT 376 380 WPAPP -> CQRHH (in Ref. 3).
CC CONFLICT 386 386 T -> G (in Ref. 3).
CC CONFLICT 405 405 T -> Q (in Ref. 2).
CC CONFLICT 453 453 H -> D (in Ref. 1).
CC CONFLICT 775 775 R -> A (in Ref. 3).
CC CONFLICT 853 853 V -> L (in Ref. 2).
CC CONFLICT 864 864 G -> N (in Ref. 2).
CC CONFLICT 931 931 D -> N (in Ref. 2).
CC SEQUENCE 1189 AA; 134715 MW; 36276B685916A0DF CRC64;
Query Match 27.4%; Score 934.5; DB 1; Length 1189;
Best local Similarity 36.3%; Pred. No. 3e-52;
Matches 242; Conservative 103; Mismatches 227; Indels 95; Gaps 27;
Qy 21 QTNHQ---YPLADNPNTLEELNYKEFLRWTEDSSTEVLN---STVKDVGTSVVG 74
Db 3 ENNQNCIPYCNLSNPEVL-----LDGERISTGNSSIDISLSLV- 42
Qy 75 QILGVGVPPAGALTSPYQSLNTWPSDADPKAFMAQVEVLIDKKIEYAKSKALAEI 134
Db 43 QFLVSNFVPGGFLUGLIDFWGLVGFPSQ---WDAFLVQEQLINERIAEFARNAIANL 99
Qy 135 QGLQNPFEDYVNALNKKTPLSLRKSRQDRIRLEFSQAESHFRNMPFSAVKFEVLV 194
Db 100 EGLNNFNIVYAEAFKEEDP---NNPATRVIDRFRILDGLERIDPSFRISGFEVPL 156
Qy 195 LPTVAQANHTLLLLKDAQVGEWGYSSSEDAFVYHRLKLTQGYTHCVNMYVGLNG 254
Db 157 LSVYAQAANLHLATLRDSVIFGERWGLTITNVNENYRLRHIDEYADHCANTYNRGLNW 216

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Qy 255 LRGSYDAVVKENRFRREMTLTVLDLILVLPFPYDIILYSKGVKTELTRDIFTDPIESLN- 313
Db 217 LPKSTYQDMITYNLRRLDLTLVIDIAAFPNVDRRYPIQPVQLTRVYTDPLINFP 276
Qy 314 TLQEYG--PTFLSIENS-IRKPHLPDYLOQIEPHTRLPQGYFGKDSFNWGSNYVETRPS 370
Db 277 QLQSVACLPTFNWMESSAIRNPHLDILNNLTIFT---DMFSVGRNFWYGGHRVIS--S 330
Qy 371 IGSKVIITSPFYG-DKSTEPVQKLSFDGQKVVYETIANTDV---AAWPNKVVYL-GVTKV 424
Db 331 LIGGGNITSPIYREANQEPFRSFTFNG-PVFTTSLNPTLRLQLQWPAPPPNLRGVEGV 389
Qy 425 DFQYDDQKNETSTQTYDKRNNGHVSQAQSIDQLPPEPTTDEPLEKAYSHQLNAYACFLM 484
Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSRLCHA---TF 434
Qy 485 QDRRGITPFP-----FTWTHRSVDFNTIDAERKITQLPVVKAYALSGASIIISGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFSTHRSATLNTIDPERINQIPLVKFRVMGTSVITGPGFTGG 493
Qy 539 NLLFLKSSNSIAKFKVTLNSAALLQRYRYRIRVASTNLRLFV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVNIINS-PITQRYLRFRYASSRDARVILVTCGAATGCGGVSVN 551
Qy 588 DFLVIYINKMKNKDDDLTYQTDFLATNSNWGFS-----GDKNELIIGAESFVSNEKIY 641
Db 552 ----MPLQKTWEIGENLTSTRFTVDFSNPFPFRANPDIIIGISQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613
RESULT 44
QYINB8
ID Q6YNB8 PRELIMINARY; PRT; 1189 AA.
AC Q6YNB8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta-endotoxin (Insecticidal protein CryIcA).
GN Name=cryIC; Synonyms=cryIcA;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A. PubMed=14629010;
RX MEDLINE=22990512; Tseng C.C., Tsai Y.S.;
RA "Kao S.S., Hsieh F.C., Tzeng C.C., Tsai Y.S.;
RT "Cloning and expression of the insecticidal crystal protein gene
RT CryIcA9 of Bacillus thuringiensis G10-01A from Taiwan granaries.";
RL Curr. Microbiol. 47:295-299(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Kao S.-S., Hsieh F.-C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=c002;
RA Chen Z., Wu X., Zhang J., Yao J., Huang D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078160; AAL79362.1; -.
DR EMBL; AF362020; AAM00264.1; -.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.

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SQ SEQUENCE 1189 AA; 134714 MW; 362768685916A0DF CRC64;
Query Match 27.4%; Score 934.5; DB 2; Length 1189;
Best Local Similarity 36.3%; Pred. No. 36-52;
Matches 242; Conservative 103; Mismatches 227; Indels 95; Gaps 27;

Qy 21 QTNHQ---YPLADNPSTLEELNKEFLRMTEDSDSTEVLN---STVKDAVGTGISVVG 74
Db 3 ENNQNCIPYCNLSNPEVL-----LDGERISTGSSIDISLSLV- 42

Qy 75 QILGVGVPPAGALTSTFYQSFLNTIWPSSDADPKAPMAQVEVLIDKKIEYAKSKALAE 134
Db 43 QFLVSNFVPGGFLVGLIDFVWGVGPSQ---WDAFLVQIEQLINERIAEFARNAATAN 99

Qy 135 QGLQNNFEDYVNALNSWKKTPLSLRKRSQDRIRLEFSQAESHFRNSMPSFAVSKPEVL 194
Db 100 EGLGNFNIVYEAPEKEEDP---NNPATRTRVIDRFRIDGLLERDIPFRISGFEVPL 156

Qy 195 LPTYQAANTHLLLLKDAQVGEWGYSEDVAEFYHRQLKLTQOYTDHCNNVYVGLNG 254
Db 157 LSVYAQAANLHLAILRDSVIFGERWGLTTINVENYNRLIRHIDEVADHCANTYNRGLN 216

Qy 255 LRSTYDAWKNFRPREMTLTVLDLIVLPPFYDIRLYSGVKTELTRDITFDPIFSLN- 313
Db 217 LPKSTYQDMITYNRLRDLTLVLDIAAFPNYDNRRIPIQPVGQLTREYITDPLINFNP 276

Qy 314 TLQEYG--PTFLSIENS-IRKPHLFDYLOGIEPHRLQPGYFGKDSFNYSWGNVETRPS 370
Db 277 QLSVAQLPTFNWESSAIRNPHLFDILNLTFT----DWFSVGRNFYWGHRVIS--S 330

Qy 371 IGSKTITSPFYG-DKSTEPVQKLSFDGQKRYRTIANTDV---AAMPNGKVYL-GYTKV 424
Db 331 LIGGGNITSPYGREANQPPRSFTFNG-PVPRTLNPTLRLQLQQPWPAPPFNLRGVEGV 389

Qy 425 DFSQYDDQKNETSTQYDSCRNGHVSQAQSDIQLPPTTDEPLEKAYSHQLYAECLFM 484
Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSHRLCHA---TF 434

Qy 485 QDRRGTIPTF-----FTWTHRSVDFNTIDAETITOLPVVKAYALSSGASIIEGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFVSWTHRSATLTNTIDPERINQIPLVKGRVWGTSVITGPGFTGG 493

Qy 539 NLLFKESSNSIAKFKVTLNSAALLQRYRIRIYASTTNLRLFV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVINS-PITQRYLRFRYASSRDARVILTGAASTGVGGQSVN 551

Qy 588 DFLVIYINKTMKDDDLTYQTFDLATNSNMGFS-----GDKNELIIGAESFVSNKIIY 641
Db 552 ----MPLQKTMETGENLTSRTF--RYTDFSNPFSFRANPDIIIGISEQPLFGAGS-ISSGELY 606

Qy 642 IDKIEFI 648
Db 607 IDKIEII 613

RESULT 45
Q9L877 PRELIMINARY; PRT; 1189 AA.
AC Q9L877;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Toxin CrylCa6.
GN Name=crylCa6;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;
RA Yu J., Pang Y., Li J.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF215647; AAF37224.1; -.
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Query Match	26.4%	Score	998.5	DB 2	Length	1156			
Best Local Similarity	33.3%	Pred. No.	6.5e-50						
Matches	220	Conservative	118	Mismatches	231	Indels	91	Gaps	24

QY	31	DNPNSTLEELNYKEFLRTWSDSSFEVLNDNSIVKDAVGTGISVVG-----QILGVVGVPF	84
Db	3	NNPNIN-ECIPY-----NCLSNPEVEVLGGERIE---TGYTPIDISLSTQFLISEFVPG	53
QY	85	AGALTSFYQGFLLNTIW----PSDADPNKFAFMAQVEVLIDKKIEYSYAKSKALAAELQGLNN	140
Db	54	AG----FVLGLVDIIWGI FGPSQ---WDAFLVQIEQLINQRIEFARNQALSRLEGLSNL	106
QY	141	FEDYVNALNSWKKTPLSLRKSRSODRTRELPSQAESHFRNSMPFAVSKFVFLPTVTAQ	200
Db	107	YQIYAESFREWEADPTN-PALREEMRIQ--FNDMNSALTTAIPFAVQNYVPLLSVVVQ	163
QY	201	AAMTHILLLLKDAQVFGGEWGYSSDDVAEFYHRQLKLTQQYTDDHCWNVNVGLNGLRGSTY	260
Db	164	AANLHLFVLDDVSVFGQWGFDAATINRSYNDLTRLIGNYTDHVRWYNTGLERVWGPD	223
QY	261	DAWVKFNRRFEMTLTVLDDIIVLFPFFYDIDRLYSKGVKTELTRDITFDPIFSLNTLQOEYGP	320

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